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THIS IS TO CERTIFY THAT ANNEXED HERETO IS A TRUE COPY FROM THE RECORDS OF THE UNITED STATES PATENT AND TRADEMARK OFFICE OF THOSE PAPERS OF THE BELOW IDENTIFIED PATENT APPLICATION THAT MET THE REQUIREMENTS TO BE GRANTED A FILING DATE UNDER 35 USC 111.

APPLICATION NUMBER: 09/514,599**FILING DATE: February 28, 2000****PRIORITY
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jc780 U.S. PTO
02/28/00

Attorney Docket No.: 6072.200-US

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

FILING UNDER 37 C.F.R. 1.53(b)

jc525 U.S. PTO
09/514599
02/28/00

Box Patent Application
Assistant Commissioner for Patents
Washington, DC 20231

Express Mail Label No. EL473439879US
Date of Deposit February 28, 2000

Sir:

This is a request for filing a patent application under 37 C.F.R. 1.53(b) of

Applicant(s): Allan Svendsen

Title: Pullulanase Variants and Methods for Preparing Such Variants With
Predetermined Properties

158 pages of specification including Abstract 1 sheets of drawings

10 pages of sequence 1-2; 10 pages of sequence 3-4; and 9 pages of sequence 5-6.

3 sheets of Declaration and Power of Attorney

[x] The filing fee is calculated as follows:

Basic Fee:	\$ 690.00
Total Claims: $39 - 20 = 19 \times 18 =$	\$ 342.00
Independent Claims: $4 - 3 = 1 \times 78 =$	\$ 78.00
Total Fee:	\$1,110.00

Priority of Danish application no. PA 2000 00045 filed on January 12, 2000 is
claimed under 35 U.S.C. 119.

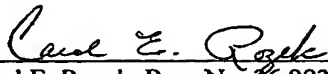
Address all future communications to Steve T. Zelson, Esq., Novo Nordisk of
North America, Inc., 405 Lexington Avenue, Suite 6400, New York, NY 10174-6401.

09514599-022800

Please charge the required fee, estimated to be \$1,110, to Novo Nordisk of North America, Inc., Deposit Account No. 14-1447. A duplicate of this sheet is enclosed.

R spectfully submitted,

Date: February 28, 2000



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02/28/00
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2-29-00

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PATENT

Attorney Docket No.: 6072.200-US

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

EXPRESS MAIL CERTIFICATE

Box Patent Application
Assistant Commissioner for Patents
Washington, DC 20231

Re: U.S. Patent Application for
Title: Pullulanase Variants and Methods for Preparing Such Variants
With Predetermined Properties
Applicants: Allan Svendsen

Sir:

Express Mail Label No. EL473439876US

Date of Deposit : February 28, 2000

I hereby certify that the following attached paper(s) or fee

1. Filing Under 37 C.F.R. 1.53(b) (in duplicate)
2. Patent Application
3. Unexecuted Combined Declaration and Power of Attorney
4. Preliminary Amendment

are being deposited with the United States Postal Service "Express Mail Post Office to Addressee" under 37 C.F.R. 1.10 on the date indicated above and is addressed to the Commissioner of Patents and Trademarks, Washington, DC 20231.

Miriam Kelly
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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Allan Svendsen

Application No.: TBA

Group Art Unit: TBA

Filed: February 28, 2000

Examiner: TBA

For: Pullulanase Variants and Methods for Preparing
Such Variants With Predetermined Properties

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents
Washington, DC 20231

Sir:

Before the above-captioned application is taken up for examination, entry of the following amendment is respectfully requested:

IN THE SPECIFICATION:

At page 1, after the title, insert

--CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims priority under 35 U.S.C. 119 of Danish application PA 2000 00045 filed January 12, 2000, the contents of which are fully incorporated herein by reference.--

At page 144, delete the heading "CLAIMS" and insert therefore --What is claimed is:--.

IN THE CLAIMS:

Cancel claims 11-14, 16-19, 24, 25, 28-32, 38, 41 and 42 without prejudice or disclaimer.

1. (Amended) A method for producing a variant of a parent pullulanase, the variant having at least one altered property as compared to the parent pullulanase, the method comprising:

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a) modeling the parent pullulanase on the three-dimensional structure of SEQ ID NO:1 [depicted in the Appendix] to produce a three-dimensional structure of the parent pullulanase;

b) identifying in the three-dimensional structure obtained in step (a) at least one structural part of the parent pullulanase, wherein an alteration in said structural part is predicted to result in an altered property;

c) modifying the nucleic acid sequence encoding the parent pullulanase to produce a nucleic acid sequence encoding a deletion, insertion, or substitution of one or more amino acids at a position corresponding to said structural part; and

d) expressing the modified nucleic acid sequence in a host cell to produce the variant pullulanase.

2. (Amended) The method [according to] of claim 1, wherein the altered property is pH dependent activity, thermostability, substrate cleavage pattern, specific activity of cleavage, substrate specificity[, such as higher isoamylase activity and/or] or substrate binding.

3. (Amended) The method [according to] of claim 2, wherein the altered property is a higher isoamylase activity as defined by an increase of at least 5% in the number of reducing ends formed in [the] an "assay for isoamylase-like activity" [described herein,] using 50 mM sodium acetate, a pH of 4.5, 5.0 or 5.5, a temperature of 60°C and when incubated with a 10% w/v rabbit liver glycogen solution for a period of 10 min.

4. (Amended) The method [according to claims 1 or 2] of claim 1, wherein the altered property is an improved thermostability as defined by differential scanning calorimetry (DSC) [using the method described herein].

5. (Amended) The method [according to claims 1 or 2] of claim 1, wherein the altered property is an improved thermostability as defined by an increased half-life ($T_{1/2}$) of at least about 5%[, preferably, at least about 10%, more preferably at least about 15%, more preferably at least about 25%, most preferably at least about 50%, such as at least about 100%, in the] in a " $T_{1/2}$ assay for liquefaction" [described herein], using a pH of 5.0 and a temperature of 95°C.

6. (Amended) The method [according to claims 1 or 2] of claim 1, wherein the altered property is an improved thermostability as defined by an increased residual enzyme activity of at least about 5%[, preferably, at least about 10%, more preferably at least about 15%, more preferably at least about 25%, most preferably at least about 50%, such as at least about 100%, in the] in an "assay for residual activity after liquefaction" [described herein], using a pH of 5.0 and a temperature of 95°C.

7. (Amended) The method [according to claims 1 or 2] of claim 1, wherein the altered property is an improved thermostability as defined by an increased half-life ($T_{1/2}$) of at least about 5%[, preferably, at least about 10%, more preferably at least about 15%, more preferably at least about 25%, most preferably at least about 50%, such as at least about 100%, in the] in a " $T_{1/2}$ assay for saccharification" [described herein], using a pH of 4.5 and a temperature of 70°C.

8. (Amended) The method [according to claims 1 or 2] of claim 1, wherein the altered property is an improved thermostability as defined by an increased residual enzyme activity of at least about 5%[, preferably, at least about 10%, more preferably at least about 15%, more preferably at least about 25%, most preferably at least about 50%, such as at least about 100%, in the] in an "assay for residual activity after saccharification" [described herein], using a pH of 4.5 and a temperature of 63°C.

9. (Amended) The method according to claim 8, wherein the "assay for activity for saccharification" [described herein], is carried out at a pH of 4.5 and at a temperature of 70°C.

10. (Amended) A method for constructing a variant of a parent pullulanase, the method comprising:

- a) identifying an internal or external cavity or crevice in [the] a three-dimensional structure of the parent pullulanase;
- b) substituting at least one amino acid residue in the neighborhood of the cavity or crevice with another amino acid residue which increases the hydrophobic interaction and/or fills out or reduces the size of the cavity or crevice;
- c) optionally repeating steps a) and b) recursively;

- d) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b);
- e) preparing the variant resulting from steps a) - d);
- f) testing the thermostability of said variant; and
- g) optionally repeating steps a) - f) recursively; and
- h) selecting a variant having increased thermostability as compared to the parent pullulanase.

15. (Amended) A method according to [any of claims 10-14] claim 10, wherein the increased thermostability is as defined in [any of claims 4-9] claim 4.

20. (Amended) A method according to [any of the preceding claims] claim 1, wherein the parent pullulanase has more than 40% homology with the amino acid sequence shown in SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5[, preferably more than 50%, such as more than 60%, more than 70%, more than 75%, more than 80%, more than 85%, more than 90%, more than 91%, more than 92%, more than 93%, more than 94%, more than 95%, more than 96%, more than 97%, more than 98%, more than 99% homology with the amino acid sequence shown in SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5].

21. (Reiterated) A method according to claim 20, wherein the parent pullulanase has the amino acid sequences shown in SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5.

22. (Amended) A method for producing a pullulanase variant, the method comprising:

- a) constructing the variant by the method according to [any of claims 10-21] claim 10;
- b) transforming a microorganism with a DNA sequence encoding the variant;
- c) cultivating the transformed microorganism under conditions which are conducive for producing the variant; and
- d) optionally, recovering the variant from the resulting culture broth.

23. (Amended) A pullulanase variant, wherein

- (a) the variant has more than 40% homology to SEQ ID NO:1;
- (b) the variant comprises an amino acid modification compared to SEQ ID NO:1 in at least one of the positions corresponding to 95-113, K122P, 130-140, K151P, 157-165, 180,

181, 210, 227, 228, 232-238, 259, 266-272, 286, G293P, 298, 299, 300-314, [such as 302-308,] N315P, 337-339, 353, N374P, 380, 384, 385, 392, 394, 396, 406, 408-429, [such as 418-428,] 442, A446P, 478, 500-507, 515, 526, 534, 543, 544 550, T556P, 557, 563, 568, 573, 576, 583, 627, 659-665, G668P, G672P, 681, 684, 688, 689, 751-755, 732, 736, 740, 760, 767, 770 783, 788, 792, 793, [such as N793P,] K758C+I914C, T916C+A765C, I897C+S819C, P525C+E499C and H286C+T148C; and

(c) the variant has an improved thermostability as compared to the parent pullulanase.

26. (Amended) [A] The pullulanase variant according to [any of claims 23, 24 or 25] claim 23, wherein the variant has more than 45% homology with the amino acid sequence shown in SEQ ID NO: 1[, preferably more than 50%, such as more than 60%, more than 70%, more than 75%, more than 80%, more than 85%, more than 90%, more than 91%, more than 92%, more than 93%, more than 94%, more than 95%, more than 96%, more than 97%, more than 98%, more than 99% homology with the amino acid sequence shown in SEQ ID NO: 1].

27. (Amended) [A] The pullulanase variant according to claim 26, wherein the parent pullulanase has the amino acid sequence shown in SEQ ID NO:1.

33. (Amended) [A] The variant according to [claims 23 or 28] claim 23, wherein the improved thermostability is defined by an increased half-life ($T_{1/2}$) of at least about 5% [, preferably, at least about 10%, more preferably at least about 15%, more preferably at least about 25%, most preferably at least about 50%, such as at least about 100%, in the] in a "T_{1/2} assay for liquefaction" [described herein], using a pH of 5.0 and a temperature of 95°C.

34. (Amended) [A] The variant according to [claims 23 or 28] claim 23, wherein the improved thermostability is defined by an increased residual enzyme activity of at least about 5% [, preferably, at least about 10%, more preferably at least about 15%, more preferably at least about 25%, most preferably at least about 50%, such as at least about 100%, in the] in an "assay for residual activity after liquefaction" [described herein] using a pH of 5.0 and a temperature of 95°C.

35. (Amended) [A] The variant according to [claims 23 or 28] claim 23, wherein the improved thermostability is defined by an increased half-life ($T_{1/2}$) of at least about 5% [, preferably, at least about 10%, more preferably at least about 15%, more preferably at least about 25%, most preferably at least about 50%, such as at least about 100%, in the] in a " $T_{1/2}$ assay for saccharification" [described herein], using a pH of 4.5 and a temperature of 70°C.
36. (Amended) [A] The variant according to [claims 23 or 28] claim 23, wherein the improved thermostability is defined by an increased residual enzyme activity of at least about 5% [, preferably, at least about 10%, more preferably at least about 15%, more preferably at least about 25%, most preferably at least about 50%, such as at least about 100%, in the] in an "assay for residual activity after saccharification" [described herein], using a pH of 4.5 and a temperature of 63°C.
37. (Amended) [A] The variant according to claim 36, wherein the "assay for activity for saccharification" [described herein,] is carried out at a pH of 4.5 and at a temperature of 70°C.
39. (Amended) [A] The variant according to [any of claims 23, 25, 28 or 30] claim 23, wherein the variant further has an increased isoamylase activity as compared to the parent pullulanase.
40. (Amended) [A] The variant according to claim 37, wherein the increased isoamylase activity is as defined in claim 38.
43. (Amended) [A] The variant according to [any of claims 23, 24, 28 or 29] claim 23, wherein the variant further has an altered pH dependent activity as compared to the parent pullulanase.
44. (Amended) An isolated nucleic acid sequence comprising a nucleic acid sequence, which encodes for the pullulanase variant defined in [any of claims 23-43] claim 23.
45. (Amended) [An] The isolated nucleic acid sequence according to claim 44, wherein the nucleic acid sequence is selected [from] from the group consisting of:

- (a) a nucleic acid sequence having at least 40% homology with the nucleic acid sequence shown in SEQ ID NO:1 or SEQ ID NO:3, and
- (b) a nucleic acid [sequence] sequence which hybridizes under [low stringency conditions, preferably under medium stringency conditions, in particular under] high stringency conditions, with
- (i) a complementary strand of the nucleic acid sequence shown in SEQ ID NO: 1 or SEQ ID NO: 3, or
 - (ii) a subsequence of (i) of at least 100 nucleotides.

46. (Amended) [An] The isolated nucleic acid sequence according to claim 45, wherein the nucleic acid sequence has at least [45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least] 99% homology with the nucleic acid sequence shown as SEQ ID NO: 1 or SEQ ID NO:3.

47. (Amended) An isolated nucleic acid construct comprising a nucleic acid sequence as defined in [any of claims 44-46] claim 44, operably linked to one or more control sequences capable of directing the expression of the polypeptide in a suitable expression host.

48. (Amended) A recombinant expression vector comprising the nucleic acid sequence of claim 47, a promoter, [and] transcriptional and translational stop signals, and [preferably further comprising] a selectable marker.

49. (Reiterated) A recombinant host cell comprising the nucleic acid construct of claim 47.

50. (Amended) A method for producing the variant defined in [any of claims 23-43] claim 23, the method comprising:

- (a) cultivating the recombinant host cell of claim 49 under conditions conducive to the production of the pullulanase variant; and
- (b) recovering the variant.

51. (Amended) A method for converting starch to one or more sugars, the method comprising debranching the starch using at least one pullulanase obtained by the [methods defined in any of claims 1-22] method of claim 1.

52. (Amended) A method for converting starch to one or more sugars, the method comprising debranching the starch using at least one pullulanase variant as defined in [any of claims 23-44] claim 23.

53. (Reiterated) An isolated nucleic acid sequence comprising the nucleic acid sequence shown in SEQ ID NO: 1.

54. (Reiterated) A nucleic acid sequence according to claim 53, wherein the isolated nucleic acid sequence consists of the nucleic acid sequence shown in SEQ ID NO: 1.

55. (Amended) An isolated nucleic acid construct comprising a nucleic acid sequence as defined in [claims 53 or 54] claim 53, operably linked to one or more control sequences capable of directing the expression of the polypeptide in a suitable expression host.

56. (Amended) A recombinant expression vector comprising the nucleic acid sequence of claim 55, a promoter, [and] transcriptional and translational stop signals, and [preferably further comprising] a selectable marker.

57. (Reiterated) A recombinant host cell comprising the nucleic acid construct of claim 55.

REMARKS

This preliminary amendment is submitted simultaneously with the filing of the present application. By this amendment, applicants have amended the specification, cancelled claims 11-14, 16-19, 24, 25, 28-32, 38, 41 and 42, and amended claims 1-10, 15, 20, 22, 23, 26, 27, 33-37, 39, 40, 43-48, 50, 51, 52, 55 and 56. The claims as now written set forth the invention in language that more fully accords with U.S. practice and rules to assist the Examiner in his or her consideration of the differences between the claimed invention and the prior art. No new matter has been added by this amendment.

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PULLULANASE VARIANTS AND METHODS FOR PREPARING SUCH VARIANTS WITH PREDETERMINED PROPERTIES

FIELD OF THE INVENTION

The present invention relates to variants of pullulanases and to methods for
5 constructing such variants.

BACKGROUND OF THE INVENTION

Starches such as corn, potato, wheat, manioc and rice starch are used as the starting
material in commercial large scale production of sugars, such as high fructose syrup,
high maltose syrup, maltodextrins, amylose, G4-G6 oligosaccharides and other
10 carbohydrate products such as fat replacers.

Degradation of starch

Starch usually consists of about 80% amylopectin and 20% amylose. Amylopectin is
a branched polysaccharide in which linear chains α -1,4 D-glucose residues are joined
by α -1,6 glucosidic linkages. Amylopectin is partially degraded by α -amylase, which
15 hydrolyzes the 1,4- α -glucosidic linkages to produce branched and linear
oligosaccharides. Prolonged degradation of amylopectin by α -amylase results in the
formation of so-called α -limit dextrins which are not susceptible to further hydrolysis
by the α -amylase. Branched oligosaccharides can be hydrolyzed into linear
oligosaccharides by a debranching enzyme. The remaining branched
20 oligosaccharides can be depolymerized to D-glucose by glucoamylase, which
hydrolyzes linear oligosaccharides into D-glucose.

Amylose is a linear polysaccharide built up of D-glucopyranose units linked together
by α -1,4 glucosidic linkages. Amylose is degraded into shorter linear
oligosaccharides by α -amylase, the linear oligosaccharides being depolymerized into
25 D-glucose by glucoamylase.

In the case of converting starch into a sugar, the starch is depolymerized. The
depolymerization process consists of a pretreatment step and two or three

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consecutive process steps, namely a liquefaction process, a saccharification process and, depending on the desired end product, optionally an isomerization process.

Pre-treatment of native starch

Native starch consists of microscopic granules which are insoluble in water at room temperature. When an aqueous starch slurry is heated, the granules swell and eventually burst, dispersing the starch molecules into the solution. During this "gelatinization" process there is a dramatic increase in viscosity. As the solids level is 30-40% in a typical industrial process, the starch has to be thinned or "liquefied" so that it can be handled. This reduction in viscosity is today mostly obtained by enzymatic degradation.

Liquefaction

During the liquefaction step, the long-chained starch is degraded into smaller branched and linear units (maltodextrins) by an α -amylase (e.g. Termamyl™, available from Novo Nordisk A/S, Denmark). The liquefaction process is typically carried out at about 105-110°C for about 5 to 10 minutes followed by about 1-2 hours at about 95°C. The pH generally lies between about 5.5 and 6.2. In order to ensure an optimal enzyme stability under these conditions, calcium is added, e.g. 1 mM of calcium (40 ppm free calcium ions). After this treatment the liquefied starch will have a "dextrose equivalent" (DE) of 10-15.

Saccharification

After the liquefaction process the maltodextrins are converted into dextrose by addition of a glucoamylase (e.g. AMG™, available from Novo Nordisk A/S) and a debranching enzyme, such as an isoamylase (see e.g. US Patent No. 4,335,208) or a pullulanase (e.g. Promozyme®, available from Novo Nordisk A/S; see US Patent No. 4,560,651). Before this step the pH is reduced to a value below 4.5, e.g. about 3.8, maintaining the high temperature (above 95°C) for a period of e.g. about 30 min. to inactivate the liquefying α -amylase to reduce the formation of short oligosaccharides

called "panose precursors" which cannot be hydrolyzed properly by the debranching enzyme.

The temperature is then lowered to 60°C, glucoamylase and debranching enzyme are added, and the saccharification process proceeds for about 24-72 hours.

- 5 Normally, when denaturing the α -amylase after the liquefaction step, a small amount of the product comprises panose precursors which cannot be degraded by pullulanases or AMG. If active amylase from the liquefaction step is present during saccharification (i.e. no denaturing), this level can be as high as 1-2% or even higher, which is highly undesirable as it lowers the saccharification yield significantly. For this
- 10 reason, it is also preferred that the α -amylase is one which is capable of degrading the starch molecules into long, branched oligosaccharides (such as, e.g., the Fungamyl™-like α -amylases) rather than shorter branched oligosaccharides.

Isomerization

- When the desired final sugar product is e.g. high fructose syrup, the dextrose syrup
- 15 may be converted into fructose by enzymatic isomerization. After the saccharification process the pH is increased to a value in the range of 6-8, preferably about pH 7.5, and the calcium is removed by ion exchange. The dextrose syrup is then converted into high fructose syrup using, e.g., an immobilized glucose isomerase (such as Sweetzyme™, available from Novo Nordisk A/S).

20 Debranching enzymes

- Debranching enzymes which can attack amylopectin are divided into two classes: isoamylases (E.C. 3.2.1.68) and pullulanases (E.C. 3.2.1.41), respectively. Isoamylase hydrolyses α -1,6-D-glucosidic branch linkages in amylopectin and β -limit dextrins and can be distinguished from pullulanases by the inability of isoamylase to
- 25 attack pullulan, and by their limited action on α -limit dextrins.

When an acidic stabilized α -amylase is used for the purpose of maintaining the amylase activity during the entire saccharification process (no inactivation), the

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degradation specificity should be taken into consideration. It is desirable in this regard to maintain the α -amylase activity throughout the saccharification process, since this allows a reduction in the amyloglucidase addition, which is economically beneficial and reduces the AMG™ condensation product isomaltose, thereby increasing the DE
5 (dextrose equivalent) yield.

It will be apparent from the above discussion that the known starch conversion processes are performed in a series of steps, due to the different requirements of the various enzymes in terms of e.g. temperature and pH. It would therefore be desirable to be able to engineer one or more of these enzymes, e.g. pullulanases, so that the
10 overall process could be performed in a more economical and efficient manner. One possibility in this regard is to engineer the otherwise thermolabile pullulanases so as to render them more stable at higher temperatures.

BRIEF DISCLOSURE OF THE INVENTION

The inventors have modified the amino acid sequence of a pullulanase to obtain
15 variants with improved properties, based on the three-dimensional structure of the pullulanase Promozyme® (available from Novo Nordisk A/S). The variants have altered physicochemical properties, e.g. an altered pH optimum, improved thermostability, increased specific activity or an altered cleavage pattern.

Accordingly, the object of the present invention is to provide a method for
20 constructing pullulanases having altered properties, in particular to provide a method for constructing pullulanases having improved thermostability, altered pH dependent activity and/or altered substrate specificity, such as increased isoamylase activity.

Thus, in its broadest aspect, the present invention relates to a method for constructing a variant of a parent pullulanase, wherein the variant has at least one
25 altered property as compared to said parent pullulanase, which method comprises:

- i) analyzing the structure of the pullulanase to identify, on the basis of an evaluation of structural considerations, at least one amino acid residue or at least one structural region of the pullulanase, which is of relevance for altering said property;

ii) constructing a variant of the pullulanase, which as compared to the parent pullulanase, has been modified in the amino acid residue or structural part identified in i) so as to alter said property; and

iii) testing the resulting pullulanase variant for said property.

5 The property which may be altered by the above methods of the present invention may be, e.g., thermostability, pH dependent activity, specific activity, or substrate specificity. Thus, the variant may have, e.g., increased thermostability, higher activity at a lower pH, an altered pH optimum, improved thermostability, or increased specific activity, such as increased isoamylase activity.

10 Although it has been described in the following that modification of the parent pullulanase in certain regions and/or positions is expected to confer a particular effect to the thus produced pullulanase variant (such as an improved thermostability or an increased isoamylase activity), it should be noted that modification of the parent pullulanase in any of such regions may also give rise to any other of the above-
15 mentioned effects. For example, any of the regions and/or positions mentioned as being of particular interest with respect to, e.g., improved thermostability, may also give rise to, e.g., higher activity at a lower pH, an altered pH optimum, or increased specific activity, such as increased isoamylase activity.

Further aspects of the present invention relates to variants of a pullulanase, the DNA
20 encoding such variants and methods of preparing the variants. Still further aspects of the present invention relates to the use of the variants for various industrial purposes, in particular for processes where sweeteners are made from starch. Other aspects of the present invention will be apparent from the below description as well as from the appended claims.

25 **BRIEF DESCRIPTION OF THE DRAWINGS**

Fig. 1 shows the DNA plasmid pCA36 harboring the gene encoding the pullulanase from *Bacillus deramificans* (SEQ ID NO: 3).

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DETAILED DISCLOSURE OF THE INVENTION

Pullulanases

As explained above, pullulanases are enzymes classified in EC 3.2.1.41 and such enzymes are characterized by their ability to hydrolyze the α -1,6-glycosidic bonds in, 5 for example, amylopectin and pullulan.

A particularly interesting pullulanase is the pullulanase from *Bacillus acidopullulyticus* described in US 4,560,651 (hereinafter referred to as Promozyme®). Promozyme® has the amino acid sequence set forth in amino acids 1-921 of SEQ ID NO: 1. The three-dimensional structure of Promozyme® is described below.

- 10 Another interesting pullulanase is the pullulanase from *Bacillus deramificans* described in US 5,736,375. This enzyme has the amino acid sequence set forth in amino acid sequence 1-928 of SEQ ID NO: 3. Homology building of the tree-dimensional structure of the above-mentioned pullulanase is described below.

In general, a preferred pullulanase suitable for the purpose described herein should 15 have one or more of the following properties:

- i) A three-dimensional structure homologous to Promozyme®.
- ii) An amino acid sequence which is at least 40% homologous to SEQ ID NO:1 or SEQ ID NO:3, preferably at least 50%, e.g. at least 60%, such as a least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at 20 least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% homologous to SEQ ID NO:1 or SEQ ID NO:3.
- iii) A nucleic acid sequence which hybridizes to the nucleic acid sequence set forth in SEQ ID NO:1 or SEQ ID NO:3.

The structural homology referred to above in i) above is based on other sequence 25 homologies, hydrophobic cluster analysis or by reverse threading (Huber, T ; Torda, AE, PROTEIN SCIENCE Vol. 7 , No. 1 pp. 142-149 (1998)) and which by any of

these methods is predicted to have the same tertiary structure as Promozyme, wherein the tertiary structure refers to the overall folding or the folding of Domains N1, N2, A, B, and C. Alternatively, a structural alignment between Promozyme and homologous sequences may be used to identify equivalent positions.

- 5 For example, the homology between various pullulanase with known amino acid sequence has been compiled in the below matrix:

	1	2	3	4	5	6	7	8	9	10
1. pula_kleae	100	86	59	51	52	53	52	52	55	50
2. pula_klep		100	58	51	51	53	53	53	53	52
10 3. w81973			100	55	56	52	55	54	51	56
4. r56989				100	98	60	76	54	56	76
5. sp929mat					100	61	78	54	57	78
6. fervido_x						100	61	57	54	62
7. sp734							100	56	54	91
15 8. r71616								100	54	56
9. w09257									100	54
10. Promozyme®										100

1. Pula_kleae: Pullulanase from *Klebsiella aerogenes* (*J. Bacteriol.* (1987) **169**, 2301-2306).
- 20 2. Pula_klep: Pullulanase from *Klebsiella pneumonia* (*Mol. Microbiol.* (1990) **4**, 73-85; *J. Bacteriol.* (1985) **164**, 639-645; *J. Bacteriol.* (1989) **171**, 3673-3679).
3. W81973: Pullulanase fragment from *zea mays* (WO 98/50562).
4. r56989: Mature pullulanase from *Bacillus deramificans* T 89.117D (EP 0 605 040).
5. sp929mat: Mature part of pullulanase from *Bacillus deramificans* (US 5,736,375).
- 25 6. fervido_x: Mature part of pullulanase from *Fervidobacterium pennavorans* Ven5 (*Appl. Environ. Microb.* (1997) **63**, 1088-1094).

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7. sp734: Mature pullulanase from *Bacillus acidopullulyticus* (FEMS Mic. Let. (1994) 115, 97-106.

8. r71616: Pullulanase from *Thermus* sp. (JP 07023783).

9. w09257: Pullulanase from *Bacillus* sp. KSM-AP 1378 (WO 96/35794).

5 The above homology calculations were determined by use of the GAP program from the UWGCG package using default values for GAP penalties, i.e. GAP creation penalty of 3.0 and GAP extension penalty of 0.1 (Program Manual for the Wisconsin Package, Version 8, August 1994, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711).

10 A sequence alignment between Promozyme® (SEQ ID NO: 1), the pullulanase from *Bacillus deramificans* (SEQ ID NO: 3) and the pullulanase from *Bacillus acidopullulyticus* (SEQ ID NO: 5) described in *FEMS Mic. Let.* (1994) **115**, 97-106, is shown in Appendix 2.

Three-dimensional structure of pullulanase

- 15 Promozyme® was used to elucidate the three-dimensional structure forming the basis for the present invention.

The structure of Promozyme® was solved in accordance with the principle for x-ray crystallographic methods, for example, as given in X-Ray Structure Determination, Stout, G.K. and Jensen, L.H., John Wiley & Sons, Inc. NY, 1989.

- 20 The structural coordinates for the solved crystal structure of Promozyme® using the isomorphous replacement method are given in standard PDB format (Protein Data Bank, Brookhaven National Laboratory, Brookhaven, CT) as set forth in Appendix 1. It is to be understood that Appendix 1 forms part of the present application. In the context of Appendix 1, the following abbreviations are used: WAT refers to water or to
25 calcium. Amino acid residues are given in their standard three letter code.

The structure of said Pullulanase is made up of five globular domains, ordered N1, N2, A, B, and C. The domains can be defined as being residues 1-310 for domain

N1, 311-420 for Domain N2, residues 421-556 and 596-835 for domain A, residues 557-595 for Domain B, residues 596-922 for Domain C, wherein the numbering refers to the amino acid sequence in SEQ ID NO: 1. Features of Domains N1, A, B and C of particular interest are described below.

5 Domain N1

Domain N1 contains in this particular pullulanase an extra loop of 100 residues compared to the pullulanase from *Bacillus acidopullulyticus* having the amino acid sequence shown in SEQ ID NO: 5. The loop is also present in the pullulanase from *Bacillus deramificans* having the amino acid sequence shown in SEQ ID NO: 3.

- 10 Part of the N2 domain is homologous to the N1 domain of Pseudomonase amyloclavata isoamylase (1bf2.pdb from Brookhaven database).

Domain A

- Domain A is the largest domain and contains the active site which comprises a cluster of three amino acid residues, D622, D736 and E651, spatially arranged at the
 15 bottom of a cleft in the surface of the enzyme. The structure of Domain A shows an overall fold in common with the α -amylases for which the structure is known, viz. the (beta/alpha) 8 barrel with eight central beta strands (numbered 1-8) and eight flanking a-helices. The β -barrel is defined by McGregor, *J. Prot. Chem.* 7:399, 1988. The C-terminal end of the beta strand 1 is connected to helix 1 by a loop denoted loop 1
 20 and an identical pattern is found for the other loops, although the loops show some variation in size and some can be quite extensive.

- The eight central beta-strands in the (beta/alpha) 8 barrel superimpose reasonably well with the known structures of family 13 (Henrissat B. *Biochem. J.* (1991) **280**, 309-316 and Henrissat B. and Bairoch A. *Biochem. J.* (1993) **293**, 781-788). This part of
 25 the structure, including the close surroundings of the active site located at the C-terminal end of the beta-strands, shows a high degree of homology with isoamylases.

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In contrast, the loops connecting the beta-strands and alpha helices display a high degree of variation from the known structures of family 13 enzymes. These loops constitute the structural context of the active site, and the majority of the contacts to the substrate is found among residues located in these loops. Distinguishing characteristics such as substrate specificity, substrate binding, pH activity profile, substrate cleavage pattern, and the like, are determined by specific amino acids and the positions they occupy in these loops.

Domain B

Domain B, also referred to as loop 3 of the (beta/alpha) 8 barrel, comprises amino acid residues 557-595 of the amino acid sequence shown in SEQ ID NO: 1. The most striking difference to other family 13 enzymes being the short amino acid sequence. This short sequence loop are of the same size as the isoamylase loop 3 and spatially positioned close to the active site residues and in close contact to the substrate.

Domain C

Domain C in Promozyme comprises amino acid residues 596-922 of the amino acid sequence shown in SEQ ID NO: 1. Domain C is composed entirely of β -strands which form a single 8-stranded sheet structure that folds back on itself, and thus may be described as a β -sandwich structure. One part of the β -sheet forms the interface to Domain A.

Substrate Binding Site

Parts of the loop discussed above in the context of domains A, B and N2 are of particular interest for substrate interaction and active site reactivity. In particular, in domain A, residues 439-443 in loop 1, residues 490-514 in loop 2, residues 621-628 in loop 4, residues 652-668 in loop 5, residues 679-694 in loop 6, residues 733-740 in loop 7 and residues 787-796 in loop 8; in domain B, residues 553-564 and 581-592 in loop 3; in domain N2, residues 400-404, wherein residue positions correspond to the amino acids in the amino acid sequence in SEQ ID NO: 1.

Homology building of *Bacillus deramificans* pullulanase or other pullulanases.

The structure of the *Bacillus deramificans* pullulanase (SEQ ID NO:3) was model built on the structure disclosed in Appendix 1 herein. The structure of other pullulanases may be built analogously.

A model structure of a pullulanase can be built using the Homology program or a comparable program, e.g., Modeller (both from Molecular Simulations, Inc., San Diego, CA). The principle is to align the sequence of the pullulanase with the known structure with that of the pullulanase for which a model structure is to be constructed. The structurally conserved regions can then be built on the basis of consensus sequences. In areas lacking homology, loop structures can be inserted, or sequences can be deleted with subsequent bonding of the necessary residues using, e.g., the program Homology. Subsequent relaxing and optimization of the structure should be done using either Homology or another molecular simulation program, e.g., CHARMM from Molecular Simulations.

Methods for designing novel pullulanase variants

In a first aspect, the present invention relates to a method for producing a variant of a parent pullulanase, wherein the variant has at least one altered property as compared to the parent pullulanase, the method comprising:

i) modeling the parent pullulanase on the three-dimensional structure of SEQ ID NO: 1 depicted in Appendix 1 to produce a three-dimensional structure of the parent pullulanase;

ii) identifying in the three-dimensional structure obtained in step (i) at least one structural part of the parent pullulanase, wherein an alteration in the structural part is predicted to result in an altered property;

iii) modifying the nucleic acid sequence encoding the parent pullulanase to produce a nucleic acid sequence encoding a deletion, insertion, or substitution of one or more amino acids at a position corresponding to the structural part; and

iv) expressing the modified nucleic acid sequence in a host cell to produce the variant pullulanase.

The structural part which is identified in step ii) of the method of the invention may be composed of one amino acid residue. Normally, however, the structural part comprises more than one amino acid residue, typically constituting one of the above-mentioned parts of the pullulanase structure such as one of the N1, N2, A, B, or C domains, an interface between any of these domains, a calcium binding site, a loop structure, the substrate binding site, or the like.

The structural or functional considerations may involve an analysis of the relevant structure or structural part and its contemplated impact on the function of the enzyme. For example, an analysis of the functional differences between pullulanases and the various isoamylases may be used for assigning certain properties of Promozyne® or homologous model builded structure to certain parts of the Promozyne® or homologous model builded structure or to contemplate such relationship. For instance, differences in the pattern or structure of loops surrounding the active site may result in differences in access to the active site of the substrate and thus differences in substrate specificity and/or cleavage pattern.

Furthermore, parts of a pullulanase involved in substrate binding, and thus, for example, substrate specificity and/or cleavage, thermostability, and the like, have been identified (*vide infra*).

The modification of an amino acid residue or structural region is typically accomplished by suitable modifications of a nucleic acid sequence encoding the parent enzyme in question. The modification may be substitution, deletion or insertion of an amino acid residue or a structural part.

The property to be modified may be stability (e.g. thermostability), pH dependent activity, substrate specificity, such as decreased condensation reactions, isoamylase like activity etc. Thus, the altered property may be an altered specific activity at a given pH and/or altered substrate specificity, such as an altered pattern of substrate cleavage or an altered pattern of substrate inhibition.

In step ii) of the method according to the invention the part of the structure to be identified is preferably one which in the folded enzyme is believed to be in contact

with the substrate (cf. the disclosure above in the section entitled "Substrate Binding Site") or involved in substrate specificity and/or cleavage pattern, and/or one which is contributing to the pH or temperature profile of the enzyme, or is otherwise responsible for the properties of the pullulanase.

- 5 Described in the following are specific types of variants which have been designed by use of the method of the invention.

The variants of the invention may comprise additional modifications in addition to the modifications described herein. The variants preferably have an amino acid sequence having more than 40% homology with SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO:

- 10 5, preferably more than 50%, e.g. more than 60%, such as more than 70%, more than 75%, more than 80%, more than 85%, more than 90%, more than 91%, more than 92%, more than 93%, more than 94%, more than 95%, more than 96%, more than 97%, more than 98% or more than 99% homology with the amino acid sequences shown in SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5.

- 15 In the present context the term "homologous to" or "homology" (also sometimes referred to as "similarity") is used in its conventional meaning and the "homology" between two amino acid sequences may be determined by use of any conventional algorithm, preferably by use of the GAP program from the UWGCG package using default values for GAP penalties, i.e. GAP creation penalty of 3.0 and GAP extension
20 penalty of 0.1 (Program Manual for the Wisconsin Package, Version 8, August 1994, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711). The method is also described in S.B. Needleman and C.D. Wunsch, *Journal of Molecular Biology*, **48**, 443-445 (1970).

- As mentioned above, the property to be modified may be stability (e.g.
25 thermostability), pH dependent activity, substrate specificity, such as increased isoamylase activity, or specific activity. Thus, the altered property may be an altered specific activity at a given pH and/or an altered substrate specificity, such as an altered pattern of substrate cleavage or an altered pattern of substrate inhibition.

In a particular interesting embodiment of the invention the property to be modified is the thermostability of the enzyme.

In the present context, the term "thermostable" (or "thermostability") refers in general to the fact that the pullulanase variants according to the invention have an improved
5 thermostability compared to the relevant parent pullulanase. The degree of improvement in thermostability can vary according to factors such as the thermostability of the parent pullulanase and the intended use of the pullulanase variant, i.e. whether it is primarily intended to be used for liquefaction or for
10 saccharification, the enzyme variant should maintain a substantial degree of enzyme activity during the saccharification step at a temperature of at least about 63°C, preferably at least about 70°C, while an enzyme variant designed for use in the liquefaction step should be able to maintain a substantial degree of enzyme activity at a temperature of at least about 95°C.

- 15 The improved thermostability of enzyme variants according to the invention can in particular be defined according to one or more of the following criteria:

In one embodiment, the pullulanase variant of the invention has an improved thermostability (and/or the method of the invention provides a pullulanase with an improved thermostability) as defined by differential scanning calorimetry (DSC) using
20 the method described herein.

In another embodiment, the pullulanase variant of the invention has an improved thermostability (and/or the method of the invention provides a pullulanase with an improved thermostability) as defined by an increased half-time ($T_{1/2}$) of at least about 5%, preferably at least about 10%, more preferably at least about 15%, more
25 preferably at least about 25%, most preferably at least about 50%, such as at least about 100%, in the " $T_{1/2}$ assay for liquefaction" described herein, using a pH of 5.0 and a temperature of 95°C. Pullulanase variants according to this definition are suitable for use in the liquefaction step of the starch conversion process.

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Alternatively or additionally, a pullulanase variant suitable for use in liquefaction can be defined as having an improved thermostability as defined by an increased residual enzyme activity of at least about 5%, preferably at least about 10%, more preferably at least about 15%, more preferably at least about 25%, most preferably at least
5 about 50%, such as at least about 100%, in the "assay for residual activity after liquefaction" described herein, using a pH of 5.0 and a temperature of 95°C.

In a further embodiment, the enzyme variant of the invention has an improved thermostability (and/or the method of the invention provides a pullulanase with an improved thermostability) as defined by an increased half-time ($T_{1/2}$) of at least about
10 5%, preferably at least about 10%, more preferably at least about 15%, more preferably at least about 25%, most preferably at least about 50%, such as at least about 100%, in the " $T_{1/2}$ assay for saccharification" described herein, using a pH of 4.5 and a temperature of 70°C. Such variants are suitable for use in the saccharification step of the starch conversion process.

15 Alternatively or additionally, a pullulanase variant suitable for saccharification can be defined as having an improved thermostability as defined by an increased residual enzyme activity of at least about 5%, preferably at least about 10%, more preferably at least about 15%, more preferably at least about 25%, most preferably at least about 50%, such as at least about 100%, in the "assay for residual activity after
20 saccharification" described herein, using a pH of 4.5 and a temperature of 63°C. Preferably, this improved thermostability is also observed when assayed at a temperature of 70°C.

The term "substantially active" as used herein for a given pullulanase variant and a given set of conditions of temperature, pH and time means that the relative enzymatic
25 activity of the enzyme variant is at least about 25%, preferably at least about 50%, in particular at least about 60%, especially at least about 70%, such as at least about 90% or 95%, e.g. at least about 99% compared to the relative activity of the parent enzyme tested under the same set of conditions.

One advantage of the thermostable pullulanase of the invention is that they make it possible to perform liquefaction and debranching simultaneously before the saccharification step. This has not previously been possible, since the known pullulanases with acceptable specific activity are thermolabile and are inactivated at 5 temperatures above 60°C. (Some thermostable pullulanases from *Pyrococcus* are known, but these have an extremely low specific activity at higher temperatures and are thus unsuitable for purposes of the present invention). By debranching, using the thermostable pullulanases of the invention, during liquefaction together with the action of an α -amylase, the formation of panose precursors is reduced, thereby 10 reducing the panose content in the final product and increasing the overall saccharification yield. It is also possible in this manner to extend the liquefaction process time without risking formation of large amount of panose precursors. By prolonging the liquefaction step, the DE yield is increased from 10-15 to e.g. 15-20, reducing the need for glucoamylase. This reduced glucoamylase requirement is in 15 turn advantageous as the formation of undesired isomaltose is reduced, thereby resulting in an increased glucose yield. In addition, the reduced glucoamylase addition enables the saccharification step to be carried out at a higher substrate concentration (higher DS, dry substances, concentration) than the normal approx. 30-35% used according to the prior art. This allows reduced evaporation costs 20 downstream, e.g. in a high fructose corn syrup process, and the saccharification reaction time can also be reduced, thereby increasing production capacity. A further advantage is that α -amylase used in the liquefaction process does not need to be inactivated/denatured in this case.

Furthermore, it is also possible to use the thermostable pullulanases of the invention 25 during saccharification, which is advantageous for several reasons. In the conventional starch saccharification process, the process temperature is not more than 60°C due to the fact that neither the saccharification enzyme pullulanase nor AMG™ are sufficiently thermostable to allow the use of a higher temperature. This is a disadvantage, however, as it would be very desirable to run the process at a temperature of above 30 about 60°C, in particular above 63°C, e.g. about 70°C, to reduce microbial growth during the relatively long saccharification step. Furthermore, a higher process

temperature normally gives a higher activity per mg of enzyme (higher specific activity), thereby making it possible to reduce the weight amount of enzyme used and/or obtain a higher total enzymatic activity. A higher temperature can also result in a higher dry matter content after saccharification, which would be beneficial in terms of reducing
5 evaporation costs.

In another interesting embodiment of the invention the property to be modified is the substrate specificity of the pullulanase, in particular to modify the substrate specificity of the pullulanase in such a way the variant pullulanase becomes more "isoamylase-like" in the sense of having an increased activity towards high molecular weight
10 branched starchy material such as glycogen and amylopectin. Methods for determining the substrate specificity of pullulanases are discussed in the following section entitled "Methods for determining stability, activity and specificity".

Thus, when used herein, the term "increased isoamylase activity" refers in general to the fact that the pullulanase variants according to the invention exhibits a higher
15 activity towards high molecular weight branched starchy material, such as glycogen and amylopectin as compared to the parent pullulanase.

The increased isoamylase activity of the pullulanase variants according to the invention can in particular be defined according to the below criteria:

In one embodiment the pullulanase variant according to the invention has an
20 increased isoamylase activity as defined by an increase of at least 5%, preferably of at least 10%, more preferably of at least 15%, more preferably of at least 25%, most preferably of at least 50%, in particular of at least 75%, such as of at least 100% in the number of reducing ends formed in the "assay for isoamylase-like activity" described herein, using 50 mM sodium acetate, a pH of 4.5, 5.0 or 5.5, a temperature
25 of 60°C and when incubated with a 10 w/v rabbit liver glycogen solution for a period of 10 min.

In the present context the term "pullulanase activity" is intended to mean that the pullulanase variant in question is capable of degrading pullulan when tested as

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described in the Examples (see the section entitled "Determination of pullulanase activity).

Methods for determining stability, activity and specificity

Thermostability

- 5 Thermostability of pullulanases can be detected by measuring the residual activity by incubating the enzyme under accelerated stress conditions, which comprise: pH 4.5 in a 50 mM sodium acetate buffer without a stabilizing dextrin matrix (such as the approximately 35% dry matter which is normally present during saccharification). The stability can be determined at isotherms of e.g. 63°C, 70°C, 80°C, 90°C and 95°C,
- 10 measuring the residual activity of samples taken from a water bath at regular intervals (e.g. every 5 or 10 min.) during a time period of 1 hour. For determining stability for the purpose of liquefaction, a pH of 5.0, a temperature of 95°C and a total assay time of 30 to 120 minutes are used ("assay for residual activity after liquefaction"). For determining stability for the purpose of saccharification, a pH of 4.5, a temperature of
- 15 63°C or 70°C and a total assay time of 30 minutes are used ("assay for residual activity after saccharification").

Alternatively, the thermostability may be expressed as a "half-time" ($T_{1/2}$), which is defined as the time, under a given set of conditions, at which the activity of the enzyme being assayed is reduced to 50% of the initial activity at the beginning of the assay. In

20 this case, the " $T_{1/2}$ assay for liquefaction" uses a pH of 5.0 and a temperature of 95°C, while the " $T_{1/2}$ assay for saccharification" uses a pH of 4.5 and a temperature of 70°C. The assay is otherwise performed as described above for the respective assays for residual activity.

Activity: Somogyi-Nelson method for determination of reducing sugars

- 25 The activity of pullulanases can be measured using the Somogyi-Nelson method for the determination of reducing sugars (*J. Biol. Chem.* **153**, 375 (1944)). This method is based on the principle that sugar reduces cupric ions to cuprous oxide, which reacts with an arsenate molybdate reagent to produce a blue colour that is measured

spectrophotometrically. The solution to be measured must contain 50-600 mg of glucose per liter. The procedure for the Somogyi-Nelson method is as follows:

Sample value: Pipet 1 ml of sugar solution into a test tube. Add 1 ml of copper reagent. Stopper the test tube with a glass bead. Place the test tube in a boiling water bath for 5 20 minutes. Cool the test tube. Add 1 ml of Nelson's color reagent. Shake the test tube without inverting it. Add 10 ml of de-ionized water. Invert the test tube and shake vigorously. Measure the absorbance at 520 nm, inverting the test tube once immediately prior to transfer of the liquid to the cuvette.

Blank value: Same procedure as for the sample value, but with water instead of sugar 10 solution.

Standard value: Same procedure as for the sample value.

Calculations: In the region 0-2 the absorbance is proportional to the amount of sugar.

$$15 \quad \text{mg sugar/l} = \frac{100 (\text{sample} - \text{blank})}{(\text{standard} - \text{blank})}$$

$$20 \quad \% \text{ glucose} = \frac{(\text{sample} - \text{blank})}{100 \times (\text{standard} - \text{blank})}$$

Reagents:

1. Somogyi's copper reagent

35.1 g $\text{Na}_2\text{HPO}_4 \cdot 2\text{H}_2\text{O}$ and 40.0 g potassium sodium tartrate ($\text{KNaC}_4\text{H}_4\text{O}_2 \cdot 4\text{H}_2\text{O}$) are dissolved in 700 ml of de-ionized water. 100 ml of 1N sodium hydroxide and 80 ml of 10% cupric sulphate ($\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$) are added. 180 g of anhydrous sodium sulphate are dissolved in the mixture, and the volume is brought to 1 liter with de-ionized water.

5 2. Nelson's color reagent

50 g of ammonium molybdate are dissolved in 900 ml of de-ionized water. Then 42 ml of concentrated sulphuric acid are added, followed by 6 g of disodium hydrogen arsenate heptahydrate dissolved in 50 ml of deionized water, and the volume is brought to 1 litre with deionized water. The solution is allowed to stand for 24-48 hours at 37°C before use and is stored in the dark in a brown glass bottle with a glass stopper.

3. Standard

100 mg of glucose (anhydrous) are dissolved in 1 liter of de-ionized water.

Alternatively, the release of reducing sugars can be measured using a 96 well plate set-up modified after Fox, J.D. & Robyt, J.F. (1991) Anal. Biochem. 195, 93-96.

15 Assay conditions are (in brief): 1 ml substrate (e.g. 1% solution) in 50 mM citric acid pH 5 is preincubated at 60 °C. A zero timepoint is taken 150 µl sample and transferred to a microtiter plate well containing 150 µl solution A + B for reducing sugar determination. The enzymatic reaction is initiated by addition of 100 µl enzyme and time points are taken at T = 1, 2, 3, 4, and 5 min.

20 After completion of the assay, the plate is developed by incubation at 85 °C for 70 minutes and the plate is read at 540 nm.

Reagents for determination of reducing value: Solution A) and solution B (62 mg copper sulfate pentahydrate and 63 mg L-serine in 50 ml water).

Pullulanase specificity

25 Methods for the determination and characterization of the profile of action and specificity of pullulanases for various substrates (e.g. amylopectin, glycogen and pullulan) are described by Kainuma et al. in *Carbohydrate Research*, 61 345-357

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(1978). Using these methods, the relative activity of a pullulanase can be determined, and the relative activity of a pullulanase variant according to the invention compared to the relative activity of the parent pullulanase can be assessed, for example to determine whether a pullulanase variant has the desired increased specificity toward
5 high molecular weight saccharides, such as amylopectin, compared to the parent pullulanase.

In order to determine whether the pullulanase variant possesses an increased isoamylase activity as compared to the parent pullulanase the following test may be performed ("assay for isoamylase-like activity"):

- 10 1000 mg rabbit liver glycogen is dissolved in 40 ml water to which 0.2% NaOH has been added. 800 mg NaBH_4 is added carefully under stirring. The solution is stirred for 48 hours at 25°C after which the reaction is stopped by addition of Amberlite IR-118H (a cation exchanger which removes the boron ions and hence stops the reaction). The solution is filtered to remove the matrix and evaporated to give 10 ml.
15 The solution is then dialyzed extensively against de-ionized water to remove residual boron ions. The parent pullulanase and the pullulanase variant are assayed according to the method of Somogyi-Nelson, using 50 mM sodium acetate, pH values of 4.5, 5.0 or 5.5 and a temperature of 60°C, with a reaction time of 10 minutes. Glucose is used as a standard, a standard curve being made from solutions containing of 0-200
20 mg glucose/liter.

Clearly, the higher the number of reducing ends formed during the incubation period, the higher "isoamylase activity". The increase in the pullulanase variant's isoamylase activity is expressed as a percentage value based on the original "isoamylase activity" of the parent pullulanase.

25 **Pullulanase variants with altered stability**

A variant with improved stability (typically increased thermostability) may be obtained by substitution with proline, substitution of histidine with another amino acid, introduction of a disulfide bond, removal of a deamidation site, altering a hydrogen bond contact, filling in an internal structural cavity with one or more amino acids with

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bulkier side groups, introduction of interdomain interactions, altering charge distribution, helix capping, or introduction of a salt bridge .

Increased mobility regions:

The following regions have an increased mobility in the crystal structure of Promozyme®, and it is presently believed that these regions can be responsible for stability or activity of the enzyme. Improvements of the enzyme can be obtained by mutation in the below regions and positions. Introducing e.g. larger residues or residues having more atoms in the side chain could increase the stability, or e.g. introduction of residues having fewer atoms in the side chain could be important for the mobility and thus the activity profile of the enzyme. The regions can be found by analysing the B-factors taken from the pdb file, and/or from molecular dynamics calculations of the isotropic fluctuations. These can be obtained by using the program CHARMM from MSI (Molecular simulations inc.).

Thus, in order to stabilize mobile regions in the structure, a preferred variant of a parent pullulanase comprises a modification, e.g. a substitution, of an amino acid residue corresponding to one or more of the following residues of the amino acid sequence set forth in SEQ ID NO: 1:

- 408-429 (i.e. 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428 and 429),
- 300-314 (i.e. 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313 and 314),
- 157-165 (i.e. 157, 158, 159, 160, 161, 162, 163, 164 and 165),
- 95-113 (i.e. 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112 and 113),
- 130-140 (i.e. 130, 131, 132, 133, 134, 135, 136, 137, 138, 139 and 140),
- 232-238 (i.e. 232, 233, 234, 235, 236, 237 and 238),

266-272 (i.e. 266, 267, 268, 269, 270, 271 and 272),

302-308 (i.e. 302, 303, 304, 305, 306, 307 and 308),

418-428 (i.e. 418, 419, 420, 421, 422, 423, 424, 425, 426, 427 and 428),

500-507 (i.e. 500, 501, 502, 503, 504, 505, 506 and 507),

5 659-665 (i.e. 659, 660, 661, 662, 663, 664 and 665) and

751-755 (i.e. 751, 752, 753, 754 and 755).

Similar modifications, e.g. substitutions, may be introduced in equivalent positions of other pullulanases. Variants of particular interest have a combination of one or more of the above with any of the other modifications disclosed herein.

- 10 For example, other preferred modifications, e.g. substitutions, which are believed to stabilized mobile regions in the structure of the pullulanase from *Bacillus deramificans*, correspond to one or more of the following residues of the amino acid sequence set forth in SEQ ID NO: 3:

406-427 (i.e. 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419,

15 420, 421, 422, 423, 424, 425, 426 and 427),

298-312 (i.e. 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311 and 312),

153-161 (i.e. 153, 154, 155, 156, 157, 158, 159, 160 and 161),

20

91-109 (i.e. 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108 and 109),

126-136 (i.e. 126, 127, 128, 129, 130, 131, 132, 133, 134, 135 and 136),

25

230-236 (i.e. 230, 231, 232, 233, 234, 235 and 236),

000000-000000

264-270 (i.e. 264, 265, 266, 267, 268, 269 and 270),

300-306 (i.e. 300, 301, 302, 303, 304, 305 and 306),

5 416-426 (i.e. 416, 417, 418, 419, 420, 421, 422, 423, 424, 425 and 426),

498-505 (498, 499, 500, 501, 502, 503, 504 and 505),

656-662 (i.e. 656, 657, 658, 659, 660, 661 and 662) and

10

749-753 (i.e. 749, 750, 751, 752 and 753).

Furthermore, it is envisaged from the structure that deletion of certain amino acid residues will confer increased stability, such as increased thermostability, to the thus
15 produced variant. Variants, which are believed to be of particular importance, comprises a deletion of amino acid residues corresponding to the following residues of the amino acid sequence set forth in SEQ ID NO: 1:

Deletion of the peptide fragment 158-275, such as a deletion starting from position 158, 159, 160 or 161 and ending at position 270, 271, 272, 273, 274 or 275, i.e. the
20 longest deletion will be deletion of the peptide fragment 158-275 and the shortest deletion will be deletion of the peptide fragment 161-270.

Other deletions which are expected to confer increased stability, such as increased thermostability, to the pullulanase variant comprises a deletion of amino acid residues corresponding to the following residues of the amino acid sequence set forth in SEQ
25 ID NO: 1:

Deletion of the peptide fragment 1-315, such as deletion of the peptide fragment 1-314, 1-313, 1-312, 1-311, 1-310, 1-309, 1-308, 1-307, 1-306, 1-305, or 1-304.

Furthermore, the following deletions are expected to confer increased stability, such as increased thermostability, to the pullulanase variant comprises a deletion of amino

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acid residues corresponding to the following residues of the amino acid sequence set forth in SEQ ID NO: 1:

Deletion of the peptide fragment 1-115, such as deletion of the peptide fragment 1-114, 1-113, 1-112, 1-111, 1-110, 1-109, 1-108, 1-107, 1-106 or 1-105.

- 5 Similar deletions may be introduced in equivalent positions of other pullulanases. Variants of particular interest have a combination of one or more of the above with any of the other modifications disclosed herein.

For example, it is envisaged that deletion of the below amino acid residues will confer increased stability, such as increased thermostability, to the thus produced variant of
10 the pullulanase from *Bacillus deramificans* (SEQ ID NO: 3):

Deletion of the peptide fragment 154-273, such as a deletion starting from position 154, 155, 156 or 157 and ending at position 268, 269, 270, 271, 272 or 273, i.e. the longest deletion will be deletion of the peptide fragment 154-273 and the shortest deletion will be deletion of the peptide fragment 157-268.

- 15 Other deletions which are expected to confer increased stability, such as increased thermostability, to the pullulanase variant comprises a deletion of amino acid residues corresponding to the following residues of the amino acid sequence set forth in SEQ ID NO: 3:

Deletion of the peptide fragment 1-313, such as deletion of the peptide fragment 1-312, 1-311, 1-310, 1-309, 1-308, 1-307, 1-306, 1-305, 1-304, or 1-303.
20

Furthermore, the following deletions are expected to confer increased stability, such as increased thermostability, to the pullulanase variant comprises a deletion of amino acid residues corresponding to the following residues of the amino acid sequence set forth in SEQ ID NO: 3:

- 25 Deletion of the peptide fragment 1-111, such as deletion of the peptide fragment 1-111, 1-110, 1-109, 1-108, 1-107, 1-106, 1-105, 1-104, 1-103, 1-102 or 1-101.

Cavities and crevices

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The structure of the pullulanase contains a number of unique internal cavities, which may contain water, and a number of crevices. In order to increase the stability, preferably the thermostability, of the pullulanase it may be desirable to reduce the number or size of cavities and crevices, e.g., by introducing one or more hydrophobic contacts, preferably achieved by introducing amino acids with bulkier side chains in the vicinity or surroundings of the cavity or crevice. For instance, the amino acid residues to be modified are those which are involved in the formation of a cavity or crevice.

In order to determine which amino acid residues of a given enzyme are involved in the formation of cavities or crevices the Connolly program is normally used (B. Lee and F.M. Richards, *J. Mol. Biol.* 55, 379-400 (1971)). The program uses a probe with a certain radius to search the external and internal surface of the protein. The smallest crevice observable in this way has the probe radius.

To analyze the solved structure of Promozyme®, a modified version of the Connolly program included in the program of INSIGHT was used. In the first step, the water molecules and the ions were removed by unmerging these atoms from the solved structure. By using the command MOLECULE SURFACE SOLVENT the solvent accessible surface area was calculated for all atoms and residues using a probe radius of 1.4 Å, and displayed graphically together with the model of the solved structure. The internal cavities are then seen as dot surfaces with no connections to the external surface.

Suggestions for specific modifications to fill out the cavities are given below. By using the homology built structures and/or comparisons based on sequence alignment, mutations for homologous structures of pullulanases can be made.

Accordingly, in a further aspect the present invention relates to a method for constructing a variant of a parent pullulanase, the method comprising:

- a) identifying an internal cavity or crevice in the three-dimensional structure of the parent pullulanase;

- b) substituting at least one amino acid residue involved in the formation of a cavity or crevice with another amino acid residue which increases the hydrophobic interaction and/or fills out or reduces the size of the cavity or crevice;
- 5 c) optionally repeating steps a) and b) recursively;
- d) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b);
- e) preparing the variant resulting from steps a) - d);
- f) testing the stability and/or the temperature dependent activity profile of the variant; and
- 10 g) optionally repeating steps a) - f) recursively; and
- h) selecting a variant having increased stability and/or an altered temperature dependent activity profile as compared to the parent pullulanase.

In a preferred embodiment of the invention the variant pullulanase provided by the above method have increased thermostability as compared to the parent pullulanase. The thermostability of a given variant may be assessed as described in the above section entitled "Methods for determining stability, activity and specificity".

It will be understood that the cavity or crevice is identified by the amino acid residues surrounding said cavity or crevice, and that modification of said amino acid residues are of importance for filling or reducing the size of the cavity or crevice. Preferably, the modification is a substitution with a bulkier amino acid residue, i.e. one with a greater side chain volume or with an increased number of atoms in the side chain. For example, all the amino acids are bulkier than Gly, whereas Tyr and Trp are bulkier than Phe. The particular amino acid residues referred to below are those which in a crystal structure have been found to flank the cavity or crevice in question.

In a preferred embodiment, the variant of a pullulanase, in order to fill, either completely or partly, cavities or crevices located internally or externally in the

structure, comprises a modification, e.g. a substitution, of an amino acid residue corresponding to one or more of the following residues of the amino acid sequence set forth in SEQ ID NO: 1:

406, 394, 568, 573 576, 563, 557, 396, 392, 515, 583, 442, 792, 767, 732, 760, 783,
5 740, 688, 478, 534, 550, 627, 314.

In a more preferred embodiment, the variant of a pullulanase comprises one or more substitutions corresponding to the following substitutions in the amino acid sequence set forth in SEQ ID NO: 1:

G406A, P394F/W/I/L, I568L/F, Y573W, T576N/L/I, S563T, T557N, A396V/L/I, V392,
10 N515M/L/I, V583I/F/L, D442Q, S792Y/F, V767Q/E/L/I, V732I/L, D760Q/E/F/Y,
L783F/Y, L740Q, D688Y/F/E/Q/R/K, L478Q/R, L534F/Y/I, M550F/Y/I/L, L627F/Y/I,
L314I.

Similar modifications, e.g. substitutions, may be introduced in equivalent positions of other pullulanases. Variants of particular interest have a combination of one or more
15 of the above with any of the other modifications disclosed herein.

For example, the variant of a pullulanase may also comprise one or more substitutions corresponding to the following substitutions in the amino acid sequence set forth in SEQ ID NO: 3:

566, 485, 487, 437, 775, 779, 551, 428, 492, 495, 392, 621, 437+503, 674+664 and
20 823.

In a more preferred embodiment, the variant of a pullulanase comprises one or more substitutions corresponding to the following substitutions in the amino acid sequence set forth in SEQ ID NO: 3:

I566A, Q485H, M487L, D437H, Q775H, E779D, V551I, I428Y/F, S492F, V495I/F/Y,
25 P392Y, L621Q, D437H+D503Y, V674+L664F and L823V.

Disulfide bonds

A variant with improved stability (typically improved thermostability) as compared to the parent pullulanase may be obtained by introducing new interdomain and intradomain contacts, such as establishing inter- or intradomain disulfide bridges.

Accordingly, a further aspect of the present invention relates to a method for
5 constructing a variant of a parent pullulanase, the method comprising:

- a) identifying in the three-dimensional structure of the parent pullulanase two or more amino acid residues which, when substituted with cysteines, are capable of forming a disulfide bond;
- b) substituting the amino acids identified in a) with cysteines;
- 10 c) optionally repeating steps a) and b) recursively;
- d) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b);
- e) preparing the variant resulting from steps a) - d);
- f) testing the stability of said variant; and
- 15 g) optionally repeating steps a) - f) recursively; and
- h) selecting a variant having increased stability as compared to the parent pullulanase.

In a preferred embodiment of the invention the variant pullulanase provided by the above method have increased thermostability as compared to the parent pullulanase.

20 The thermostability of a given variant may be assessed as described in the above section entitled "Methods for determining stability, activity and specificity".

In order to determine, in the three-dimensional structure of the parent pullulanase, the amino acid residues which, when substituted with cysteines, are capable of forming a disulfide bond, residues with CB atoms less than 4Å from each other, and where the
25 direction of the CA-CB from each residue is pointing towards the other residue are

identified. Following the above-mentioned guidelines, the below amino acid residues were identified in the amino acid sequence of SEQ ID NO: 1, and it is contemplated that these residues are suitable for cystein replacement, thereby opening up the possibility of establishing one or more disulfide bridges in the variant pullulanase:

5 K758C+I914C, T916C+A765C, I897C+S819C, P525C+E499C, H286C+T148C.

Similar substitutions may be introduced in equivalent positions of other pullulanases. Variants of particular interest have a combination of one or more of the above with any of the other modifications disclosed herein.

For example, it is contemplated that the following residues, identified in the amino
10 acid sequence of the pullulanase from *Bacillus deramificans* (SEQ ID NO: 3), are suitable for cystein replacement, thereby opening up the possibility of establishing one or more disulfide bridges in the variant pullulanase:

K756C/I912C, M914C/A763C, V895C/G817C, A523C/E497C, H284C/T144C.

Surface charge distribution

15 A variant with improved stability (typically improved thermostability) as compared to the parent pullulanase may be obtained by changing the surface charge distribution of the pullulanase. For example, when the pH is lowered to about 5 or below histidine residues typically become positively charged and, consequently, unfavorable electrostatic interactions on the protein surface may occur. By engineering the
20 surface charge of the pullulanase one may avoid such unfavorable electrostatic interactions which in turn leads to a higher stability of the pullulanase.

Therefore, a further aspect of the present invention relates to method for constructing a variant of a parent pullulanase, the method comprising:

25 a) identifying, on the surface of the parent pullulanase, at least one amino acid residue selected from the group consisting of Asp, Glu, Arg, Lys and His;

- b) substituting, on the surface of the parent pullulanase, at least one amino acid residue selected from the group consisting of Asp, Glu, Arg, Lys and His with an uncharged amino acid residue;
- c) optionally repeating steps a) and b) recursively;
- 5 d) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b);
- e) preparing the variant resulting from steps a) - d);
- f) testing the stability of said variant; and
- g) optionally repeating steps a) - f) recursively; and
- 10 h) selecting a variant having increased stability as compared to the parent pullulanase.

As will be understood by the skilled person it may also, in some cases, be advantageous to substitute an uncharged amino acid residue with an amino acid residue bearing a charge or, alternatively, it may in some cases be advantageous to

15 substitute an amino acid residue bearing a charge with an amino acid residue bearing a charge of opposite sign. Thus, the above-mentioned method may easily be employed by the skilled person also for these purposes. In the case of substituting an uncharged amino acid residue with an amino acid residue bearing a charge the above-mentioned method may be employed the only difference being steps a) and b)

20 which will then read:

- a) identifying, on the surface of the parent pullulanase, at least one uncharged amino acid residue;
- b) substituting, on the surface of the parent pullulanase, at least one uncharged amino acid residue with a charged amino acid residue selected from the group
- 25 consisting of Asp, Glu, Arg, Lys and His.

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Also in the case of changing the sign of an amino acid residue present on the surface of the pullulanase the above method may be employed. Again, compared to the above method, the only difference being steps a) and b) which, in this case, read:

- a) identifying, on the surface of the parent pullulanase, at least one charged amino acid residue selected from the group consisting of Asp, Glu, Arg, Lys and His;
- b) substituting, on the surface of the parent pullulanase, at least one charged amino acid residue identified in step a) with an amino acid residue having an opposite charge.

Thus, Asp may be substituted with Arg, Lys or His; Glu may be substituted with Arg, Lys or His; Arg may be substituted with Asp or Glu; Lys may be substituted with Asp or Glu; and His may be substituted with Asp or Glu.

In a preferred embodiment of the invention the variant pullulanase provided by the above method(s) have increased thermostability as compared to the parent pullulanase. The thermostability of a given variant may be assessed as described in the above section entitled "Methods for determining stability, activity and specificity".

In order to determine the amino acid residues of a pullulanase, which are present on the surface of the enzyme, the surface accessible area are measured using the DSSP program (Kabsch and Sander, *Biopolymers* (1983), **22**, 2577-2637). All residues having a surface accessibility higher than 0 is regarded a surface residue.

The amino acid residues found on the surface of Promozyme® using the above method are as follows:

E526, Q544, E760, N338, N228, N181,

and it is contemplated that the following substitutions are of particular interest:

E526H, Q544E, E760Q, N338K/R, N228DE/, N181K/R.

Similar substitutions may be introduced in equivalent positions of other pullulanases. Variants of particular interest have a combination of one or more of the above with any of the other modifications disclosed herein.

For example, the variant of a pullulanase may also comprise one or more
5 modifications, e.g. substitutions, corresponding to the following substitutions in the amino acid sequence set forth in SEQ ID NO: 3:

444, 530, 710 and 855.

In a more preferred embodiment, the variant of a pullulanase comprises one or more substitutions corresponding to the following substitutions in the amino acid sequence
10 set forth in SEQ ID NO: 3:

D444R/K, K530Y/F/L, N710R and T855K.

Other modifications

Variants with improved stability, in particular variants with improved thermostability, can be obtained by improving existing or introducing new interdomain or intradomain
15 contacts. Such improved stability can be achieved by the modifications listed below.

Thus, one preferred embodiment of the invention relates to a variant of a parent pullulanase which has an improved stability and one or more salt bridges as compared to the parent pullulanase, wherein said variant comprises a modifications, e.g. a substitution, in a position corresponding to at least one of the following sets of
20 positions in SEQ ID NO: 1:

301, 385, 298, 299, 385 and 299+385, in particular L301R, N385R, H298R, N299R, N385D and N299R+N385D.

Similar modifications, e.g. substitutions, may be introduced in equivalent positions of other pullulanases. Variants of particular interest have a combination of one or more
25 of the above with any of the other modifications disclosed herein.

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For example, it is contemplated that the following substitutions in the pullulanase having the amino acid sequence set forth in SEQ ID NO: 3 will enhance the stability of the enzyme: T891D, S892K, T891D+S892K and N400R.

In another preferred embodiment, the variant of the pullulanase comprises a
5 substitution corresponding to one or more of the following substitutions with proline in
the amino acid sequence set forth in SEQ ID NO: 1:

G293P, K151P, K122P, N315P, N374P, N793P, A446P, G672P, G668P, T556P

In a further interesting embodiment of the invention, the variant of the pullulanase comprises a substitution corresponding to one or more of the following substitutions
10 with proline in the amino acid sequence set forth in SEQ ID NO: 3;

D562P, G794P, G292P, D148P, N119P, D314P, N373P, N792P, G671P, G667P and T554P.

Analogously, it may be preferred that one or more histidine residue(s) present in the parent pullulanase is (are) substituted with a non-histidine residues such as Y, V I, L, F, M, E, Q, N, or D. Accordingly, in another preferred embodiment, the variant of the parent pullulanase comprises a substitution of an amino acid residue corresponding to one or more of the following residues of the amino acid sequence set forth in SEQ ID NO: 3: H422Y/F/L, H483Y/F/L, H543Y/F/L/N and H613Y/F/L.

It may be preferred that one or more asparagine or glutamine residues present in the parent pullulanase is or are substituted with a residue lacking the amide group on the side chain. Preferably, such asparagines or glutamine residues are substituted with S, T, V, L and/or F amino acid residues. Accordingly, in another preferred embodiment, the variant of the parent pullulanase comprises a modification, e.g. a substitution, of an amino acid residue corresponding to one or more of the following residues of the amino acid sequence set forth in SEQ ID NO: 1:

Q543, Q339, N337, Q380, Q353, N384, N286, N298, N227, Q227, Q210, N180, Q259, N583, N790, N793, N505, N788, N736, N684, N689 or N681, preferably Q543S/T/V/L/F, Q339S/T/V/L/F, N337S/T/V/L/F, Q380S/T/V/L/F, Q353S/T/V/L/F,

N384S/T/V/L/F, N286S/T/V/L/F, N298S/T/V/L/F, N227S/T/V/L/F, Q227S/T/V/L/F, Q210S/T/V/L/F, N180S/T/V/L/F, Q259S/T/V/L/F, N583S/T/V/L/F, N790S/T/V/L/F, N793S/T/V/L/F, N505S/T/V/L/F, N788S/T/V/L/F, N736S/T/V/L/F, N684S/T/V/L/F, N689S/T/V/L/F and N681S/T/V/L/F.

- 5 The corresponding residues found in the pullulanase from *Bacillus deramificans* (SEQ ID NO: 3) include:

N400, N446, N504, N717, N735 and N789, preferably N400S/T/V/L/F, N446S/T/V/L/F, N504S/T/V/L/F, N717S/T/V/L/F, N735S/T/V/L/F and N789S/T/V/L/F.

- Moreover, it is contemplated that modifications, e.g. substitutions, in the region linking
 10 the N2 and the A domain, as well as other regions linking other domains, will confer additional stability, such as an increased thermostability, to the enzyme. Thus, in an interesting embodiment of the invention, the pullulanase variant comprises one or more modifications, e.g. substitutions, in the domain-linking regions (e.g. the region linking the N2 and A domains).

- 15 Examples of such modifications include one or more of the following substitutions in the pullulanase from *Bacillus deramificans* (SEQ ID NO: 3):

111, 112,

158-160 (i.e. 158, 159 and 160),

270-274 (i.e. 270, 271, 272, 273 and 274),

- 20 302-314 (i.e. 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313 and 314) and

408-426 (i.e. 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425 and 426).

- Examples of specific substitutions are: S111T/V/L, N112S/T/Q, S158Y/F/T,
 25 L159Y/K/R/A/S/T, G160A/S/T, D270E/S/T, L271V/I, V272I, T273N/D/E/Y/F, V274I, N302V/L/Y, N305V/L/Y, S306T/V, Q308K/R/A/S/T, Y309F, Y310E/D/Q/N/L/V/I,

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D314A/S/T, L409N, D408S/T, A410S/T, D413R/K/S/T, A415S/T, G416S/T/V, N418A/V/S/T, S419D/N/T, K421E/Q/S/T/V/A, H422D/L/Y/F, I423L/V/S/T/N/Q, T424S/A and K426A/S/T.

Other substitutions which are considered of particular importance in SEQ ID NO:3
5 include D437N and D440N.

Similar modifications, e.g. substitutions, may be introduced in equivalent positions of other pullulanases. Modifications of particular interest are any combination of one or more of the above with any of the other modifications disclosed herein.

Before actually constructing a pullulanase variant to achieve any of the above
10 objectives, it may be convenient to evaluate whether or not the contemplated amino acid modification can be accommodated into pullulanase structure, e.g. in a model of the three-dimensional structure of the parent pullulanase.

Pullulanase variants with an altered substrate specificity

One aim of the present invention is to change the degradation characteristics of a
15 pullulanase. Thus, as Promozyme® (and pullulanases in general) exhibits a low activity towards high molecular weight branched starchy material, such as glycogen and amylopectin, it may be desirable to change this cleavage pattern, e.g. so as to obtain a higher activity against such substrates, in particular when the pullulanase is to be added during the liquefaction process.

20 An altered substrate specificity may be achieved by modifying the substrate binding area in a parent pullulanase.

Accordingly, the present invention also relates to a method for constructing a variant of a parent pullulanase, the method comprising:

- 25 a) identifying the substrate binding area in a model of the three-dimensional structure of the parent pullulanase;
- b) modifying the substrate binding area by an amino acid substitution, deletion and/or insertion;

- c) optionally repeating step b) recursively;
- d) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b),
- e) preparing the variant resulting from steps a) - d);
- 5 f) testing the substrate specificity of the variant;
- g) optionally repeating steps a) - f) recursively; and
- h) selecting a variant having an altered substrate specificity as compared to the parent pullulanase.

The substrate binding area may easily be identified by homology to other family 13
 10 members. The active site residues are identified by homology. The substrate-binding site is identified by the concave cavity containing the active site residues. A substrate model is docked into the cavity. A suitable substrate model is the substrate structure found in the pdb file 1BAG termed GLC. This model can be "docked" into the Promozyme X-ray structure or a modeled Pullulanase 3D structure by superimposing
 15 the active site residues in the two structures. In 1BAG one of the active site residues has been mutated into an Gln instead of the native Glu. The active site residues to be superimposed are: D269, Q208 and D176 (1BAG) with D736, E651 and D622 (Promozyme®). The superposition can be made using the program INSIGHTII.

Without being limited to any theory, it is presently believed that binding between a
 20 substrate and an enzyme is supported by favorable interactions found within a sphere 10 Å from the substrate molecule, in particular within a sphere of 6 Å from the substrate molecule. Examples of such favorable bonds are hydrogen bonds, strong electrostatic interaction and/or hydrophobic interactions. The following residues of Promozyme® (SEQ ID NO: 1), are within a distance of 10 Å from the "docked"
 25 substrate and thus believed to be involved in interactions with said substrate:

437, 439, 487, 489, 490, 514, 679, 681, 684, 685, 731, 775, 786,

494-496 (i.e. 494, 495 and 496),

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505-511 (i.e. 505, 506, 507, 508, 509, 510 and 511),

551-559 (i.e. 551, 552, 553, 554, 555, 556, 557, 558 and 559),

584-590 (i.e. 584, 585, 586, 587, 588, 589 and 590),

620-626 (i.e. 620, 621, 622, 623, 624, 625, 626),

5 650-658 (i.e. 659, 651, 652, 653, 654, 655, 656, 657 and 658),

665-668 (i.e. 666, 667 and 668),

690-693 (i.e. 690, 691, 692 and 693),

734-738 (i.e. 734, 735, 736, 737 and 738) and

789-795 (i.e. 789, 790, 791, 792, 793, 794 and 795).

10 The following residues of Promozyme® are within a distance of 6 Å from the substrate and thus believed to be involved in interactions with said substrate:

489, 551, 553, 555, 556, 620, 651, 691, 692, 791, 793, 794,

506-510 (i.e. 507, 508, 509 and 510),

586-588 (i.e. 586, 587 and 588),

15 622-624 (i.e. 622, 623 and 624),

653-656 (i.e. 653, 654, 655 and 656) and

735-737 (i.e. 735, 736 and 737),

In a preferred embodiment of the invention, the parent pullulanase is modified in such a way that the variant pullulanase exhibits an increased isoamylase activity compared
20 to the parent pullulanase.

When used herein, the term "increased isoamylase activity" refers in general to the fact that the pullulanase variants according to the invention exhibits a higher activity

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towards high molecular weight branched starchy material, such as glycogen and amylopectin as compared to the parent pullulanase, cf. above.

In an interesting embodiment of the invention the pullulanase variant has an increased isoamylase activity as defined by an increase of at least 5%, preferably of at least 10%, more preferably of at least 15%, more preferably of at least 25%, most preferably of at least 50%, in particular of at least 75%, such as of at least 100% in the number of reducing ends formed in the "assay for isoamylase-like activity" described herein, using 50 mM sodium acetate, a pH of 4.5, 5.0 or 5.5, a temperature of 60°C and when incubated with a 10 w/v rabbit liver glycogen solution for a period of 10 min.

Similar modifications may be introduced in equivalent positions of other pullulanases. Substitutions of particular interest are any combination of one or both of the above with any of the other modifications disclosed herein.

For example, the following residues of the pullulanase from *Bacillus deramificans* 15 (SEQ ID NO: 3) are within a distance of 10 Å from the “docked” substrate and thus believed to be involved in interactions with said substrate:

435, 437, 485, 487, 488, 512, 677, 679, 682, 683, 729, 773, 784,

492-494 (i.e. 492, 493 and 494),

20

503-509 (i.e. 503, 504, 505, 506, 507, 508 and 509),

549-557 (i.e. 549, 550, 551, 552, 553, 554, 555, 556 and 557).

25 582-588 (i.e. 582, 583, 584, 585, 586, 587 and 588),

618-624 (i.e. 618, 619, 620, 621, 622, 623 and 624).

648-656 (648, 649, 650, 651, 652, 653, 654, 655 and 656),

663-666 (i.e. 663, 664, 665 and 666),

688-691 (i.e. 688, 689, 690 and 691),

5 732-736 (732, 733, 734, 735 and 736) and

787-793 (i.e. 787, 788, 879, 790, 791, 792 and 793).

The following residues of the pullulanase from *Bacillus deramificans* (SEQ ID NO: 3)
10 are within a distance of 6 Å from the substrate and thus believed to be involved in
interactions with said substrate:

487, 549, 551, 553, 554, 618, 649, 689, 690, 789, 791, 792,

504-508 (i.e. 504, 505, 506, 507 and 508),

15

584-586 (i.e. 584, 585 and 586),

620-622 (i.e. 620, 621 and 622),

20 651-654 (i.e. 651, 652, 653 and 654) and

733-735 (i.e. 733, 734 and 735).

Examples of specific modifications in the above-mentioned regions of *Bacillus*
25 *deramificans* are: L621I/V, D508M/N/L/T/V, T586I/L/V, T677W/F/Y, Y729F/I/L,
D679G/A/V, S732V/T/L/I, N735G/L/V/I/S/T/A and Δ (688-691).

Pullulanase variants with altered pH dependent activity profile

The pH dependent activity profile can be changed by changing the pKa of residues
30 within 15 Å, in particular by changing the pKa of residues within 10 Å, from the active

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site residues of the parent pullulanase. Changing the pKa of the active site residues is achieved, e.g., by changing the electrostatic interaction or hydrophobic interaction between functional groups of amino acid side chains of a given amino acid residue and its close surroundings. To obtain a higher activity at a higher pH, negatively charged residues are placed near a hydrogen donor acid, whereas positively charged residues placed near a nucleophilic acid will result in higher activity at low pH. Also, a decrease in the pKa can be obtained by reducing the accessibility of water or increasing hydrophobicity of the environment.

It is preferred that the variant in question exhibits a pH optimum which is at least about 0.5 pH units higher or lower, preferably at least about 1.0 pH units higher or lower, than the corresponding pH optimum of the parent pullulanase when tested on a suitable substrate (e.g. pullulan, amylopectin or glycogen).

Furthermore, it is particular preferred that the variant in question exhibits an increased activity in the pH range of from 4 to 5.5 as compared to the parent pullulanase when tested on a suitable substrate (e.g. pullulan, amylopectin or glycogen).

Thus, another aspect of the present invention relates to a method for constructing a variant of a parent pullulanase, the method comprising:

- a) identifying an amino acid residue which is within 15 Å, in particular within 10 Å, from an active site residue of the parent pullulanase in the three-dimensional structure of said parent pullulanase, and which is involved in electrostatic or hydrophobic interactions with an active site residue;
- b) substituting said amino acid residue with another amino acid residue which changes the electrostatic and/or hydrophobic surroundings of an active site residue, and which can be accommodated in the structure;
- c) optionally repeating steps a) and b) recursively;
- d) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b);

- e) preparing the variant resulting from steps a) - d);
- f) testing the pH dependent activity of said variant; and
- g) optionally repeating steps a) - f) recursively; and
- h) selecting a variant having an altered pH dependent activity as compared to the
5 parent amylase.

In general, an amino acid residue which is within 15 Å or 10Å, respectively, from an active site residue of the parent pullulanase may be identified by using the INSIGHTII program.

In a preferred embodiment, the variant of a parent pullulanase having an altered pH
10 dependent activity profile as compared to the parent pullulanase comprises a modification, e.g. a substitution, of an amino acid residue corresponding to one or more of the following residues of the amino acid sequence set forth in SEQ ID NO: 1 (all within 15Å from the active site residues D736, E651, D622):

430, 433, 518, 521, 565, 599, 600, 610, 611, 635, 636, 639, 717, 760, 763, 764, 767,
15 817,

435-443 (i.e. 435, 436, 437, 438, 439, 440, 441, 442, and 443),

486-496 (i.e. 486, 487, 488, 489, 490, 491, 492, 493, 494, 495 and 496),

505-515 (i.e. 505, 506, 507, 508, 509, 510, 511, 512, 513, 514 and 515),

548-560 (i.e. 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559 and 560),

20 573-575, (i.e. 573, 574 and 575),

583-595 (i.e. 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594 and 594),

602-604 (i.e. 602, 603 and 604),

606-608 (i.e. 606-607 and 608),

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616-633 (i.e. 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, and 633),

646-672 (i.e. 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671 and 672),

5 674-696 (i.e. 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695 and 696),

720-722 (i.e. 720, 721 and 722),

725-747 (i.e. 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746 and 747),

10 773-781 (i.e. 773, 774, 775, 776, 777, 778, 779, 780 and 781),

783-797 (i.e. 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796 and 797) and

799-802 (i.e. 799, 800, 801 and 802).

Within 10Å from the active site residues D736, E651, D622:

15 437, 442, 492, 514, 575, 594, 603, 632, 635, 684, 688, 691, 692, 721, 727, 729, 742, 743, 775, 777, 778, 780, 784, 786, 800,

487-490 (i.e. 487, 488, 489 and 490),

507-511 (i.e. 507, 508, 509, 510 and 511),

550-557 (i.e. 550, 551, 552, 553, 554, 555, 556 and 556),

20 585-588 (i.e. 585, 586, 587 and 588),

590-592 (i.e. 590, 591 and 592),

619-628 (i.e. 619, 620, 621, 622, 623, 624, 625, 626, 627 and 628),

648-655 (i.e. 648, 649, 650, 651, 652, 653, 654 and 655),

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665-671 (i.e. 665, 666, 667, 668, 669, 670 and 671),

676-681 (i.e. 676, 677, 678, 679, 680 and 681),

731-740 (i.e. 731, 732, 733, 734, 735, 736, 737, 738, 739 and 740) and

788-793 (i.e. 788, 789, 790, 791, 792 and 793).

- 5 Similar modifications may be introduced in equivalent positions of other pullulanases. Variants of particular interest have a combination of one or more of the above with any of the other modifications disclosed herein.

Thus, in another preferred embodiment, the variant of a parent pullulanase having an altered pH dependent activity profile as compared to the parent pullulanase

- 10 comprises a modification, e.g. a substitution, of an amino acid residue corresponding to one or more of the following residues of the amino acid sequence set forth in SEQ ID NO: 3 (all within 15 Å from the active site residues D734, E649 and D620):

428, 431, 516, 519, 563, 597, 598, 608, 609, 633, 634, 637, 715, 758, 761, 762, 765,
15 815,

433-441 (i.e. 433, 434, 435, 436, 437, 438, 439, 440 and 441),

484-494 (i.e. 484, 485, 486, 487, 488, 489, 490, 491, 492, 493 and 494),

20

503-513 (i.e. 503, 504, 505, 506, 507, 508, 509, 510, 511, 512 and 513),

546-558 (546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557 and 558),

25 571-573 (i.e. 571, 572 and 573),

581-593 (i.e. 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592 and 593),

600-602 (i.e. 600, 601 and 602),

604-606 (i.e. 604, 605 and 606),

614-631 (i.e. 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627,
5 628, 629, 630 and 631),

644-670 (i.e. 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669 and 670),

10 672-694 (i.e. 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693 and 694),

718-720 (i.e. 718, 719 and 720),

15 723-745 (i.e. 723, 734, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744 and 745).

771-779 (i.e. 771, 772, 773, 774, 775, 776, 777, 778 and 779),

20 781-795 (i.e. 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794
and 795) and

797-800 (i.e. 797, 798, 799 and 800).

25 Within 10 Å from the active site residues D734, E649 and D620:

435, 440, 490, 512, 573, 601, 605, 630, 669, 682, 686, 689, 690, 719, 725, 727, 740,
741, 773, 775, 776, 778, 782, 784, 798,

485–488 (i.e. 485, 486, 487 and 488).

505-509 (i.e. 505, 506, 507, 508 and 509),

548-555 (i.e. 548, 549, 550, 551, 552, 553, 554 and 555).

583-586 (i.e. 583, 584, 585 and 586),

588-590 (i.e. 588, 589 and 590).

617-626 (i.e. 616, 617, 618, 619, 620, 621, 622, 623, 624, 625 and 626),

5 646-653 (i.e. 646, 647, 648, 649, 650, 651, 652 and 653),

663-667 (i.e. 663, 664, 665, 666 and 667).

674-679 (i.e. 674, 675, 676, 677, 678 and 679),

729-738 (i.e. 729, 730, 731, 732, 733, 734, 735, 736, 737 and 738) and

786-791 (i.e. 786, 787, 788, 789, 790 and 791).

10 Specific examples of substitutions in the above-mentioned positions include D437L/I/V/F, D440L/I/V/F, M486K, M487K, D503L/I/V/F, D508N/L/T/V, T586V/I, M630H and D437L/I/V/F+D440L/I/V/F+D503L/I/V/F.

Nomenclature for amino acid modifications

The nomenclature used herein for defining modifications is essentially as described in WO 92/05249. Thus, G406A indicates a substitution of the amino acid G (Gly) in position 406 with the amino acid A (Ala). G406 indicates a substitution of the amino acid G (Gly) with any other amino acid. P394F/W/I/L indicates a substitution of P394 with F, W, I or L. Δ(688-691) indicates a deletion of amino acids in positions 688-691. 412-A-413 indicates an insertion of A between amino acids 412 and 413.

20 When used herein, the term "modification" (of a particular amino acid residue) is intended to cover substitution and deletion (of the particular amino acid residue) as well as insertion of one or more amino acid residues after the particular amino acid residue.

Polypeptide sequence homology

For purposes of the present invention, the degree of homology may be suitably determined according to the method described in S.B. Needleman and C.D. Wunsch, *Journal of Molecular Biology*, **48**, 443-45, with the following settings for polypeptide sequence comparison: GAP creation penalty of 3.0 and GAP extension penalty of 5 0.1. The determination may be done by means of a computer program known such as GAP provided in the UWGCG program package (Program Manual for the Wisconsin Package, Version 8, August 1994, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711).

Hybridization

- 10 Suitable experimental conditions for determining hybridization between a nucleotide probe and a homologous DNA or RNA sequence involves presoaking of the filter containing the DNA fragments or RNA to hybridize in 5x SSC (sodium chloride/sodium citrate, Sambrook, et al. *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor, 1989) for 10 min, and prehybridization of the filter in a 15 solution of 5x SSC, 5x Denhardt's solution (Sambrook, et al., 1989), 0.5% SDS and 100 µg/ml of denatured sonicated salmon sperm DNA (Sambrook, et al., 1989), followed by hybridization in the same solution containing a random-primed (A. P. Feinberg B. and Vogelstein, *Anal. Biochem.* **132**, 6-13 (1983)), ³²P-dCTP-labeled (specific activity > 1 x 10⁹ cpm/µg) probe for 12 hours at ca. 45°C. The filter is then 20 washed twice for 30 minutes in 2x SSC, 0.5% SDS at least 55°C (low stringency), preferably at least 60°C (medium stringency), more preferably at least 65°C (medium/high stringency), more preferably at least 70°C (high stringency), even more preferably at least 75°C (very high stringency).

Molecules which hybridize to the oligonucleotide probe under these conditions are 25 detected by exposure to x-ray film.

Methods of preparing pullulanase variants according to the invention

Cloning a DNA sequence encoding a pullulanase

The DNA sequence encoding a parent pullulanase may be isolated from any cell or microorganism producing the pullulanase in question, using various methods well known in the art.

First, a genomic DNA and/or cDNA library should be constructed using chromosomal
5 DNA or messenger RNA from the organism that produces the pullulanase to be studied. Then, if the amino acid sequence of the pullulanase is known, homologous, labelled oligonucleotide probes may be synthesised and used to identify pullulanase-encoding clones from a genomic library prepared from the organism in question. Alternatively, a labelled oligonucleotide probe containing sequences homologous to a
10 known pullulanase gene could be used as a probe to identify pullulanase-encoding clones, using hybridization and washing conditions of lower stringency.

Alternatively, the DNA sequence encoding the enzyme may be prepared synthetically by established standard methods, e.g. the phosphoroamidite method described by S.L. Beaucage and M.H. Caruthers, *Tetrahedron Letters*, 22, 1859-1869 (1981) or
15 the method described by Matthes et al. *The EMBO*, 3, 801-805 (1984). In the phosphoroamidite method, oligonucleotides are synthesized, e.g. in an automatic DNA synthesizer, purified, annealed, ligated and cloned in appropriate vectors.

Finally, the DNA sequence may be of mixed genomic and synthetic origin, mixed synthetic and cDNA origin or mixed genomic and cDNA origin, prepared by ligating
20 fragments of synthetic, genomic or cDNA origin, wherein the fragments correspond to various parts of the entire DNA sequence, in accordance with techniques well known in the art. The DNA sequence may also be prepared by polymerase chain reaction (PCR) using specific primers, for instance as described in US 4,683,202 or R.K. Saiki et al. *Science*, 239, 487-491(1988).

25 Site-directed Mutagenesis

Once a pullulanase-encoding DNA sequence has been isolated, and desirable sites for modification identified, modifications may be introduced using synthetic oligonucleotides. These oligonucleotides contain nucleotide sequences flanking the desired modification sites; mutant nucleotides are inserted during oligonucleotide

synthesis. In a specific method, a single-stranded gap of DNA, bridging the pullulanase-encoding sequence, is created in a vector carrying the pullulanase gene. Then the synthetic nucleotide, bearing the desired modification, is annealed to a homologous portion of the single-stranded DNA. The remaining gap is then filled in
5 with DNA polymerase I (Klenow fragment) and the construct is ligated using T4 ligase. A specific example of this method is described in Morinaga et al. *Biotechnology* 2, 639-646 (1984). US 4,760,025 discloses the introduction of oligonucleotides encoding multiple modifications by performing minor alterations of the cassette. However, an even greater variety of modifications can be introduced at any
10 one time by the Morinaga method because a multitude of oligonucleotides, of various lengths, can be introduced.

Another method of introducing modifications into a pullulanase-encoding DNA sequences is described in Nelson and Long *Analytical Biochemistry*, **180**, 147-151 (1989). It involves a 3-step generation of a PCR fragment containing the desired
15 modification introduced by using a chemically synthesized DNA strand as one of the primers in the PCR reactions. From the PCR-generated fragment, a DNA fragment carrying the modification may be isolated by cleavage with restriction endonucleases and reinserted into an expression plasmid.

Random Mutagenesis

20 Random mutagenesis is suitably performed either as localized or region-specific random mutagenesis in at least three parts of the gene translating to the amino acid sequence shown in question, or within the whole gene.

The random mutagenesis of a DNA sequence encoding a parent pullulanase may be conveniently performed by use of any method known in the art.

25 In relation to the above, a further aspect of the present invention relates to a method for generating a variant of a parent pullulanase, wherein the variant exhibits an altered property, such as increased thermostability, increased stability at low pH and at low calcium concentration, relative to the parent pullulanase, the method comprising:

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- (a) subjecting a DNA sequence encoding the parent pullulanase to random mutagenesis,
- (b) expressing the mutated DNA sequence obtained in step (a) in a host cell, and
- (c) screening for host cells expressing a pullulanase variant which has an altered
5 property relative to the parent pullulanase.

Step (a) of the above method of the invention is preferably performed using doped primers.

For instance, the random mutagenesis may be performed by use of a suitable physical or chemical mutagenizing agent, by use of a suitable oligonucleotide, or by
10 subjecting the DNA sequence to PCR generated mutagenesis. Furthermore, the random mutagenesis may be performed by use of any combination of these mutagenizing agents. The mutagenizing agent may, e.g., be one which induces transitions, transversions, inversions, scrambling, deletions, and/or insertions.

Examples of a physical or chemical mutagenizing agent suitable for the present
15 purpose include ultraviolet (UV) irradiation, hydroxylamine, N-methyl-N'-nitro-N-nitrosoguanidine (MNNG), O-methyl hydroxylamine, nitrous acid, ethyl methane sulphonate (EMS), sodium bisulphite, formic acid, and nucleotide analogues. When such agents are used, the mutagenesis is typically performed by incubating the DNA sequence encoding the parent enzyme to be mutagenized in the presence of the
20 mutagenizing agent of choice under suitable conditions for the mutagenesis to take place, and selecting for mutated DNA having the desired properties.

When the mutagenesis is performed by the use of an oligonucleotide, the oligonucleotide may be doped or spiked with the three non-parent nucleotides during the synthesis of the oligonucleotide at the positions which are to be changed. The
25 doping or spiking may be done so that codons for unwanted amino acids are avoided. The doped or spiked oligonucleotide can be incorporated into the DNA encoding the pullulaase enzyme by any published technique, using e.g. PCR, LCR or any DNA polymerase and ligase as deemed appropriate.

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Preferably, the doping is carried out using "constant random doping", in which the percentage of wild-type and modification in each position is predefined. Furthermore, the doping may be directed toward a preference for the introduction of certain nucleotides, and thereby a preference for the introduction of one or more specific amino acid residues. The doping may be made, e.g., so as to allow for the introduction of 90% wild type and 10% modifications in each position. An additional consideration in the choice of a doping scheme is based on genetic as well as protein-structural constraints. The doping scheme may be made by using the DOPE program which, *inter alia*, ensures that introduction of stop codons is avoided (L.J. Jensen et al. *Nucleic Acid Research*, **26**, 697-702 (1998).

When PCR-generated mutagenesis is used, either a chemically treated or non-treated gene encoding a parent pullulanase enzyme is subjected to PCR under conditions that increase the misincorporation of nucleotides (Deshler 1992; Leung et al., *Technique*, **1**, 1989, pp. 11-15).

A mutator strain of *E. coli* (Fowler et al., *Molec. Gen. Genet.*, **133**, 1974, 179-191), *S. cerevisiae* or any other microbial organism may be used for the random mutagenesis of the DNA encoding the pullulanase by, e.g., transforming a plasmid containing the parent enzyme into the mutator strain, growing the mutator strain with the plasmid and isolating the mutated plasmid from the mutator strain. The mutated plasmid may be subsequently transformed into the expression organism.

The DNA sequence to be mutagenized may conveniently be present in a genomic or cDNA library prepared from an organism expressing the parent pullulanase. Alternatively, the DNA sequence may be present on a suitable vector such as a plasmid or a bacteriophage, which as such may be incubated with or otherwise exposed to the mutagenising agent. The DNA to be mutagenized may also be present in a host cell either by being integrated in the genome of said cell or by being present on a vector harbored in the cell. Finally, the DNA to be mutagenized may be in isolated form. It will be understood that the DNA sequence to be subjected to random mutagenesis is preferably a cDNA or a genomic DNA sequence.

In some cases it may be convenient to amplify the mutated DNA sequence prior to performing the expression step b) or the screening step c). Such amplification may be performed in accordance with methods known in the art, the presently preferred method being PCR-generated amplification using oligonucleotide primers prepared
5 on the basis of the DNA or amino acid sequence of the parent enzyme.

Subsequent to the incubation with or exposure to the mutagenising agent, the mutated DNA is expressed by culturing a suitable host cell carrying the DNA sequence under conditions allowing expression to take place. The host cell used for this purpose may be one which has been transformed with the mutated DNA
10 sequence, optionally present on a vector, or one which was carried the DNA sequence encoding the parent enzyme during the mutagenesis treatment. Examples of suitable host cells are the following: gram positive bacteria such as *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus lentus*, *Bacillus brevis*, *Bacillus stearothermophilus*, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus coagulans*, *Bacillus*
15 *circulans*, *Bacillus lautus*, *Bacillus megaterium*, *Bacillus thuringiensis*, *Streptomyces lividans* or *Streptomyces murinus*; and gram negative bacteria such as *E. coli*.

The mutated DNA sequence may further comprise a DNA sequence encoding functions permitting expression of the mutated DNA sequence.

Localized random mutagenesis

20 The random mutagenesis may be advantageously localized to a part of the parent pullulanase in question. This may, e.g., be advantageous when certain regions of the enzyme have been identified to be of particular importance for a given property of the enzyme, and when modified are expected to result in a variant having improved properties. Such regions may normally be identified when the tertiary structure of the
25 parent enzyme has been elucidated and related to the function of the enzyme.

The localized, or region-specific, random mutagenesis is conveniently performed by use of PCR generated mutagenesis techniques as described above or any other suitable technique known in the art. Alternatively, the DNA sequence encoding the part of the DNA sequence to be modified may be isolated, e.g., by insertion into a

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suitable vector, and said part may be subsequently subjected to mutagenesis by use of any of the mutagenesis methods discussed above.

General method for random mutagenesis by use of the DOPE program

The random mutagenesis may be carried out by the following steps:

- 5 1. Select regions of interest for modification in the parent enzyme
2. Decide on mutation sites and non-mutated sites in the selected region
3. Decide on which kind of mutations should be carried out, e.g. with respect to the desired stability and/or performance of the variant to be constructed
4. Select structurally reasonable mutations
- 10 5. Adjust the residues selected by step 3 with regard to step 4.
6. Analyze by use of a suitable dope algorithm the nucleotide distribution.
7. If necessary, adjust the wanted residues to genetic code realism, e.g. taking into account constraints resulting from the genetic code, e.g. in order to avoid introduction of stop codons; the skilled person will be aware that some codon
- 15 combinations cannot be used in practice and will need to be adapted
8. Make primers
9. Perform random mutagenesis by use of the primers
10. Select resulting pullulanase variants by screening for the desired improved properties.
- 20 Suitable dope algorithms for use in step 6 are well known in the art. One such algorithm is described by Tomandl, D. et al., 1997, Journal of Computer-Aided Molecular Design 11:29-38. Another algorithm is DOPE (Jensen, LJ, Andersen, KV, Svendsen, A, and Kretzschmar, T (1998) Nucleic Acids Research 26:697-702).

Expression of pullulanase variants

The construction of the variant of interest is accomplished by cultivating a microorganism comprising a DNA sequence encoding the variant under conditions which are conducive for producing the variant, and optionally subsequently
5 recovering the variant from the resulting culture broth. This is described in detail further below.

According to the invention, a DNA sequence encoding the variant produced by methods described above, or by any alternative methods known in the art, can be expressed, in the form of a protein or polypeptide, using an expression vector which
10 typically includes control sequences encoding a promoter, operator, ribosome binding site, translation initiation signal, and, optionally, a repressor gene or various activator genes.

The recombinant expression vector carrying the DNA sequence encoding an pullulanase variant of the invention may be any vector which may conveniently be
15 subjected to recombinant DNA procedures, and the choice of vector will often depend on the host cell into which it is to be introduced. Thus, the vector may be an autonomously replicating vector, i.e. a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g. a plasmid, a bacteriophage or an extrachromosomal element, minichromosome or an
20 artificial chromosome. Alternatively, the vector may be one which, when introduced into a host cell, is integrated into the host cell genome and replicated together with the chromosome(s) into which it has been integrated.

In the vector, the DNA sequence should be operably connected to a suitable promoter sequence. The promoter may be any DNA sequence which shows
25 transcriptional activity in the host cell of choice and may be derived from genes encoding proteins either homologous or heterologous to the host cell. Examples of suitable promoters for directing the transcription of the DNA sequence encoding a pullulanase variant of the invention, especially in a bacterial host, are the promoter of the *lac* operon of *E.coli*, the *Streptomyces coelicolor* agarase gene *dagA* promoters,

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the promoters of the *Bacillus licheniformis* α -amylase gene (*amyL*), the promoters of the *Bacillus stearothermophilus* maltogenic amylase gene (*amyM*), the promoters of the *Bacillus amyloliquefaciens* α -amylase (*amyQ*), the promoters of the *Bacillus subtilis* *xylA* and *xylB* genes, etc. For transcription in a fungal host, examples of
5 useful promoters are those derived from the gene encoding *A. oryzae* TAKA amylase, *Rhizomucor miehei* aspartic proteinase, *A. niger* neutral α -amylase, *A. niger* acid stable α -amylase, *A. niger* glucoamylase, *Rhizomucor miehei* lipase, *A. oryzae* alkaline protease, *A. oryzae* triose phosphate isomerase or *A. nidulans* acetamidase.

The expression vector of the invention may also comprise a suitable transcription
10 terminator and, in eukaryotes, polyadenylation sequences operably connected to the DNA sequence encoding the pullulanase variant of the invention. Termination and polyadenylation sequences may suitably be derived from the same sources as the promoter.

The vector may further comprise a DNA sequence enabling the vector to replicate in
15 the host cell in question. Examples of such sequences are the origins of replication of plasmids pUC19, pACYC177, pUB110, pE194, pAMB1 and pIJ702.

The vector may also comprise a selectable marker, e.g. a gene the product of which complements a defect in the host cell, such as the *dal* genes from *B. subtilis* or *B. licheniformis*, or one which confers antibiotic resistance such as ampicillin, kanamycin,
20 chloramphenicol or tetracycline resistance. Furthermore, the vector may comprise *Aspergillus* selection markers such as *amdS*, *argB*, *niaD* and *sC*, a marker giving rise to hygromycin resistance, or the selection may be accomplished by co-transformation, e.g. as described in WO 91/17243.

While intracellular expression may be advantageous in some respects, e.g. when
25 using certain bacteria as host cells, it is generally preferred that the expression is extracellular. In general, the *Bacillus* α -amylases mentioned herein comprise a pre-region permitting secretion of the expressed protease into the culture medium. If desirable, this preregion may be replaced by a different preregion or signal sequence,

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conveniently accomplished by substitution of the DNA sequences encoding the respective preregions.

The procedures used to ligate the DNA construct of the invention encoding the pullulanase variant, the promoter, terminator and other elements, respectively, and to
5 insert them into suitable vectors containing the information necessary for replication, are well known to persons skilled in the art (cf., for instance, Sambrook et al. Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor, 1989).

The cell of the invention, either comprising a DNA construct or an expression vector of the invention as defined above, is advantageously used as a host cell in the
10 recombinant production of a pullulanase variant of the invention. The cell may be transformed with the DNA construct of the invention encoding the variant, conveniently by integrating the DNA construct (in one or more copies) in the host chromosome. This integration is generally considered to be an advantage as the DNA sequence is more likely to be stably maintained in the cell. Integration of the DNA
15 constructs into the host chromosome may be performed according to conventional methods, e.g. by homologous or heterologous recombination. Alternatively, the cell may be transformed with an expression vector as described above in connection with the different types of host cells.

The cell of the invention may be a cell of a higher organism such as a mammal or an
20 insect, but is preferably a microbial cell, e.g. a bacterial or a fungal (including yeast) cell.

Examples of suitable bacteria are gram positive bacteria such as *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus lentus*, *Bacillus brevis*, *Bacillus stearothermophilus*, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus coagulans*, *Bacillus*
25 *circulans*, *Bacillus lautus*, *Bacillus megaterium*, *Bacillus thuringiensis*, or *Streptomyces lividans* or *Streptomyces murinus*, or gram negative bacteria such as *E.coli*. The transformation of the bacteria may, for instance, be effected by protoplast transformation or by using competent cells in a manner known *per se*.

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Testing of pullulanase

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on the following procedure: A microorganism capable of expressing the mutated pullulanase of interest is incubated on a suitable medium and under suitable conditions for secretion of the enzyme, the medium being covered with two filters comprising a protein-binding filter placed under a second filter exhibiting a low protein binding capability. The microorganism is grown on the second, top filter. Subsequent to the incubation, the bottom protein-binding filter comprising enzymes secreted from the microorganism is separated from the second filter comprising the microorganism. The protein-binding filter is then subjected to screening for the desired enzymatic activity, and the corresponding microbial colonies present on the second filter are identified. The first filter used for binding the enzymatic activity may be any protein-binding filter, e.g., nylon or nitrocellulose. The second filter carrying the colonies of the expression organism may be any filter that has no or low affinity for binding proteins, e.g., cellulose acetate or Durapore™.

Screening consists of treating the first filter to which the secreted protein is bound with a substrate that allows detection of the activity. The enzymatic activity may be detected by a dye, fluorescence, precipitation, pH indicator, IR-absorbance or any other known technique for detection of enzymatic activity. The detecting compound may be immobilized by any immobilizing agent e.g. agarose, agar, gelatine, polyacrylamide, starch, filter paper, cloth; or any combination of immobilizing agents. For example, isoamylase activity can be detected by Cibacron Red labelled amylopectin, which is immobilized in agarose. isoamylase activity on this substrate produces zones on the plate with reduced red color intensity (clearing zones).

To screen for variants with increased stability, the filter with bound pullulanase variants can be pretreated prior to the detection step described above to inactivate variants that do not have improved stability relative to the parent pullulanase. This inactivation step may consist of, but is not limited to, incubation at elevated temperatures in the presence of a buffered solution at any pH from pH 2 to 12, and/or in a buffer containing another compound known or thought to contribute to altered stability e.g., surfactants, EDTA, EGTA, wheat flour components, or any other relevant additives. Filters so treated for a specified time are then rinsed briefly in

deionized water and placed on plates for activity detection as described above. The conditions are chosen such that stabilized variants show increased enzymatic activity relative to the parent after incubation on the detection media.

To screen for variants with altered thermostability, filters with bound variants are
5 incubated in buffer at a given pH (e.g., in the range from pH 2-12) at an elevated temperature (e.g., in the range from 50°-110°C) for a time period (e.g., from 1-20 minutes) to inactivate nearly all of the parent pullulanase, rinsed in water, then placed directly on a detection plate containing immobilized Cibacron Blue labeled pullulan and incubated until activity is detectable. As will be understood, thermostability and
10 increased isoamylase activity may be tested simultaneously by using a detection plate containing immobilized Cibacron Red labeled amylopectin and incubate until activity is detectable. Moreover, pH dependent stability can be screened for by adjusting the pH of the buffer in the above inactivation step such that the parent pullulanase is inactivated, thereby allowing detection of only those variants with
15 increased stability at the pH in question. To screen for variants with increased calcium-dependent stability, calcium chelators, such as ethylene glycol-bis(β -aminoethyl ether) N,N,N',N'-tetraacetic acid (EGTA), is added to the inactivation buffer at a concentration such that the parent pullulanase is inactivated under conditions further defined, such as buffer pH, temperature or a specified length of
20 incubation.

The variants of the invention may be suitably tested by assaying the pullulan- or amylopectin-degrading activity of the variant, for instance by growing host cells transformed with a DNA sequence encoding a variant on a starch-containing agarose plate and identifying pullulan- and/or amylopectin-degrading host cells as described
25 above. Further testing in regard to altered properties, including specific activity, substrate specificity, cleavage pattern, thermoactivation, thermostability, pH dependent activity or optimum, pH dependent stability, temperature dependent activity or optimum, transglycosylation activity, stability, and any other parameter of interest, may be performed on purified variants in accordance with methods known in
30 the art as described below.

The invention is further illustrated with reference to the following examples which are not intended to be in any way limiting to the scope of the invention as claimed.

EXAMPLES

Determination of pullulanase activity

- 5 Endo-pullulanase activity in NPUN is measured relative to a Novo Nordisk pullulanase standard. One pullulanase unit (NPUN) is defined as the amount of enzyme which releases 1 mmol glucose per minute under the standard conditions (0.7% red pullulan, pH 5, 40°C, 20 minutes). The activity is measured in NPUN/ml using red pullulan.
- 10 1 ml diluted sample or standard is incubated at 40°C for 2 minutes. 0.5 ml 2% red pullulan, 0.5 M KCl, 50 mM citric acid, pH 5 are added and mixed. The tubes are incubated at 40°C for 20 minutes and stopped by adding 2.5 ml 80% ethanol. The tubes are left standing at room temperature for 10-60 minutes followed by centrifugation 10 minutes at 4000 rpm. OD of the supernatants is then measured at
- 15 510 nm and the activity calculated using a standard curve.

Expression of pullulanase from *Bacillus deramificans*

- The pullulanase from *Bacillus deramificans* (SEQ ID NO: 3) is expressed in *B. subtilis* from a plasmid denoted pCA36. This plasmid contains the complete gene encoding the pullulanase, the expression of which is directed by the promoter from *Bacillus*
- 20 *amyloliquefaciens* α -amylase. Further, the plasmid contains the origin of replication, *oriT*, from plasmid pUB110 and the *cat* gene from plasmid pC194 conferring resistance towards chloramphenicol. PCA36 is shown in Fig. 1.

Example 1: Construction of *Bacillus deramificans* D620A variant

- Gene specific primer 132011 and mutagenic primer 132012 are used to amplify by
- 25 PCR an approximately 410 bp DNA fragment from the pCA36 plasmid.

The mutagenesis primer 132012 introduced the D620A substitution (written in bold in the primer seq.) and introduced simultaneously a Bgl I restriction site (underlined in the primer seq.), which facilitates easy pinpointing of mutants.

Finally, DNA sequencing was carried out to verify the presence of the correct mutations on the plasmid.

5' CGCTTCGGAATCATTAGGATTGC 3'

5' GCTTCCGTTTTGCCTTAATGGCGCTGC 3'

5' GGCCAAGGCTCTACCCGAACGGC 3'

20 This variant constructed as described in Example 1, except that mutagenic primer 132013 is used. The mutagenesis primer 132013 introduced the E649A substitution (written in bold in the primer seq.) and a Nar I restriction site(underlined in the primer seq.), which facilitates easy pinpointing of mutants.

Primer 132013:

5' GCACTTTACGGGGCGCCATGGACGGG 3'

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NDIX 1

1	N	PRO A 112	80.159	5.264	-8.274	1.00 42.79	71.739	-7.589	1.00 20.09
2	CA	PRO A 112	79.045	4.605	-7.604	1.00 41.43	71.932	-6.424	1.00 18.77
3	C	PRO A 112	79.488	3.326	-6.903	1.00 39.90			
4	O	PRO A 112	80.510	2.695	-7.236	1.00 39.13			
5	CB	PRO A 112	78.020	4.300	-8.676	1.00 43.58			
6	CG	PRO A 112	78.845	4.164	-9.902	1.00 42.58			
7	CD	PRO A 112	79.947	5.166	-9.749	1.00 43.50			
8	N	SER A 113	78.659	2.987	-5.901	1.00 36.72			
9	CA	SER A 113	79.034	1.812	-5.120	1.00 35.45			
10	C	SER A 113	77.884	0.992	-4.544	1.00 33.99			
11	O	SER A 113	76.732	1.456	-4.501	1.00 33.34			
12	CB	SER A 113	79.793	2.427	-3.932	1.00 36.77			
13	CG	SER A 113	78.763	3.023	-3.107	1.00 37.94			
14	N	VAL A 114	78.232	-0.222	-4.096	1.00 30.90			
15	CA	VAL A 114	77.141	-0.914	-3.375	1.00 31.03			
16	C	VAL A 114	77.274	-0.292	-1.972	1.00 29.16			
17	O	VAL A 114	76.389	-0.274	-1.420	1.00 31.09			
18	CB	VAL A 114	77.417	-2.419	-3.553	1.00 31.41			
19	CG1	VAL A 114	76.525	-3.253	-2.635	1.00 30.36			
20	O	CG2	VAL A 114	77.488	-3.080	-4.917	1.00 30.56		
21	N	SER A 115	76.266	0.401	-1.479	1.00 27.09			
22	CA	SER A 115	76.390	1.084	-0.183	1.00 25.38			
23	C	SER A 115	76.091	0.149	0.997	1.00 24.90			
24	O	SER A 115	76.347	0.637	2.117	1.00 24.00			
25	CB	SER A 115	75.558	2.373	-0.187	1.00 22.64			
26	OG	SER A 115	74.201	2.001	-0.328	1.00 22.77			
27	N	ASN A 116	75.460	-0.989	0.840	1.00 23.19			
28	CA	ASN A 116	75.223	-1.897	1.968	1.00 22.52			
29	C	ASN A 116	74.830	-3.257	1.420	1.00 21.30			
30	O	ASN A 116	74.230	-3.250	0.354	1.00 20.56			
31	CB	ASN A 116	74.117	-1.373	2.895	1.00 23.16			
32	CG	ASN A 116	74.004	-2.136	4.191	1.00 21.84			
33	OD1	ASN A 116	74.777	-1.866	5.122	1.00 20.82			
34	NO2	ASN A 116	73.090	-3.093	4.280	1.00 20.73			
35	N	ALA A 117	75.230	-4.313	2.098	1.00 19.74			
36	CA	ALA A 117	74.843	-5.672	1.740	1.00 19.18			
37	C	ALA A 117	74.602	-6.504	3.002	1.00 20.75			
38	O	ALA A 117	75.366	-6.467	3.957	1.00 21.21			
39	CB	ALA A 117	75.831	-6.457	0.873	1.00 17.81			
40	N	TYR A 118	73.479	-7.242	2.937	1.00 19.90			
41	CA	TYR A 118	73.080	-8.099	4.042	1.00 20.50			
42	C	TYR A 118	72.917	-9.549	3.578	1.00 19.26			
43	O	TYR A 118	72.422	-9.839	2.494	1.00 22.33			
44	CB	TYR A 118					71.739	-7.589	1.00 20.09
45	CG	TYR A 118					71.932	-6.424	1.00 18.77
46	CD1	TYR A 118					73.008	-6.394	6.361
47	CD2	TYR A 118					70.931	-5.460	5.586
48	CE1	TYR A 118					73.073	-5.426	7.355
49	CE2	TYR A 118					70.987	-4.499	6.586
50	CZ	TYR A 118					72.050	-4.480	7.470
51	OH	TYR A 118					72.116	-3.520	8.458
52	N	LEU A 119					73.396	-10.483	4.417
53	CA	LEU A 119					73.089	-11.871	4.133
54	C	LEU A 119					71.822	-12.293	4.863
55	O	LEU A 119					71.801	-12.501	6.070
56	CB	LEU A 119					74.257	-12.745	4.571
57	CG	LEU A 119					74.043	-14.215	4.193
58	CD1	LEU A 119					73.879	-14.416	2.682
59	CD2	LEU A 119					75.196	-15.116	4.624
60	N	ASP A 120					70.677	-12.315	4.183
61	CA	ASP A 120					69.372	-12.510	4.811
62	C	ASP A 120					68.815	-13.933	4.760
63	O	ASP A 120					67.794	-14.173	5.449
64	CB	ASP A 120					68.314	-11.512	4.346
65	CG	ASP A 120					68.469	-10.114	4.912
66	OD1	ASP A 120					69.040	-9.909	5.994
67	OD2	ASP A 120					68.000	-9.132	4.295
68	N	ASP A 121					69.459	-14.847	4.069
69	CA	ASP A 121					69.009	-16.253	4.082
70	C	ASP A 121					70.291	-17.036	3.749
71	O	ASP A 121					71.251	-16.347	3.404
72	CB	ASP A 121					67.838	-16.599	3.188
73	CG	ASP A 121					67.081	-17.860	3.551
74	OD1	ASP A 121					65.897	-17.937	3.106
75	OD2	ASP A 121					67.552	-18.838	4.190
76	N	GLU A 122					70.312	-18.167	3.847
77	CA	GLU A 122					71.613	-19.020	3.562
78	C	GLU A 122					72.181	-18.700	2.193
79	O	GLU A 122					73.415	-18.680	2.060
80	CB	GLU A 122					71.517	-20.512	3.625
81	CG	GLU A 122					70.813	-21.249	2.597
82	CD	GLU A 122					70.644	-22.717	3.015
83	OE1	GLU A 122					71.596	-23.371	3.499
84	OE2	GLU A 122					69.534	-23.235	2.779
85	N	LVS A 123					71.395	-18.480	1.147

86	CA	LVS A 123	71.909	-18.121	-0.170	1.00	22.79	131	CA	LEU A 129	73.115	0.531	-4.714	1.00	29.81
87	C	LVS A 123	71.247	-16.879	-0.755	1.00	22.17	132	C	LEU A 129	73.067	2.052	-4.625	1.00	30.79
88	O	LVS A 123	71.137	-16.788	-1.992	1.00	22.07	133	O	LEU A 129	71.997	2.621	-4.412	1.00	29.69
89	CB	LVS A 123	71.655	-19.103	-1.115	1.00	24.69	134	CB	LEU A 129	72.693	0.064	-6.092	1.00	29.38
90	CG	LVS A 123	72.497	-20.528	-0.798	1.00	27.82	135	CG	LEU A 129	72.670	-1.425	-6.455	1.00	29.89
91	CD	LVS A 123	71.837	-21.782	-1.305	1.00	30.95	136	CD	LEU A 129	72.293	-1.585	-7.931	1.00	30.38
92	CE	LVS A 123	72.745	-22.985	-1.438	1.00	33.61	137	CD2	LEU A 129	74.009	-2.112	-6.236	1.00	28.39
93	NZ	LVS A 123	71.885	-24.227	-1.408	1.00	38.51	138	N	SER A 130	74.162	2.782	-4.801	1.00	32.54
94	N	THR A 124	70.862	-15.914	0.062	1.00	18.31	139	CA	SER A 130	74.086	4.228	-4.641	1.00	34.33
95	CA	THR A 124	70.223	-14.686	-0.397	1.00	19.05	140	C	SER A 130	73.299	4.884	-5.773	1.00	36.79
96	C	THR A 124	70.918	-13.424	0.117	1.00	19.03	141	O	SER A 130	73.009	6.074	-5.768	1.00	37.29
97	O	THR A 124	71.042	-13.313	1.342	1.00	18.19	142	CB	SER A 130	75.512	4.788	-4.600	1.00	33.55
98	CB	THR A 124	68.759	-14.614	0.096	1.00	19.49	143	OG	SER A 130	76.227	4.352	-5.759	1.00	34.68
99	CG1	THR A 124	68.093	-15.853	-0.273	1.00	21.02	144	N	MET A 131	72.979	4.059	-6.795	1.00	37.15
100	CG2	THR A 124	67.958	-13.436	-0.417	1.00	17.02	145	CA	MET A 131	72.225	4.581	-7.925	1.00	39.70
101	N	VAL A 125	71.114	-12.463	-0.717	1.00	18.66	146	C	MET A 131	71.602	3.473	-8.788	1.00	38.38
102	CA	VAL A 125	71.852	-11.220	-0.221	1.00	20.11	147	O	MET A 131	72.036	2.331	-8.785	1.00	36.96
103	C	VAL A 125	70.971	-10.047	-0.698	1.00	20.51	148	CB	MET A 131	73.143	5.484	-8.760	1.00	42.16
104	O	VAL A 125	70.485	-10.031	-1.819	1.00	21.45	149	CG	MET A 131	74.218	4.719	-9.540	1.00	44.07
105	CB	VAL A 125	73.343	-10.945	-0.302	1.00	22.08	150	SD	MET A 131	74.661	5.555	-11.071	1.00	48.37
106	CG1	VAL A 125	74.227	-12.123	-0.759	1.00	21.11	151	CE	MET A 131	76.298	6.126	-10.590	1.00	45.57
107	CG2	VAL A 125	73.756	-9.615	-0.901	1.00	19.94	152	N	PRO A 132	70.445	3.644	-9.407	1.00	38.54
108	N	LEU A 126	70.757	-9.068	0.176	1.00	19.28	153	CA	PRO A 132	69.715	2.529	-9.985	1.00	38.36
109	CA	LEU A 126	69.973	-7.883	-0.113	1.00	19.43	154	C	PRO A 132	70.487	1.983	-11.172	1.00	39.15
110	C	LEU A 126	70.940	-6.717	-0.189	1.00	20.40	155	O	PRO A 132	71.420	2.615	-11.696	1.00	39.25
111	O	LEU A 126	71.583	-6.433	0.840	1.00	17.65	156	CB	PRO A 132	68.348	3.076	-10.341	1.00	39.31
112	CB	LEU A 126	68.962	-7.679	1.033	1.00	19.40	157	CG	PRO A 132	68.452	4.555	-10.271	1.00	39.22
113	CG	LEU A 126	68.214	-6.352	0.939	1.00	21.05	158	CD	PRO A 132	69.703	4.916	-9.513	1.00	39.47
114	CD1	LEU A 126	67.147	-6.379	-0.146	1.00	17.96	159	N	MET A 133	70.115	0.773	-11.554	1.00	38.46
115	CD2	LEU A 126	67.643	-5.843	2.254	1.00	18.86	160	CA	MET A 133	70.680	0.062	-12.683	1.00	37.37
116	N	ALA A 127	71.204	-6.161	-1.360	1.00	20.21	161	C	MET A 133	69.465	-0.615	-13.315	1.00	38.14
117	CA	ALA A 127	72.232	-5.138	-1.506	1.00	23.09	162	O	MET A 133	68.403	-0.628	-12.657	1.00	38.27
118	C	ALA A 127	71.665	-3.800	-1.965	1.00	24.49	163	CB	MET A 133	71.752	-0.962	-12.320	1.00	36.83
119	O	ALA A 127	70.837	-3.785	-2.898	1.00	24.26	164	CG	MET A 133	71.329	-2.070	-11.385	1.00	35.87
120	CB	ALA A 127	73.302	-5.630	-2.495	1.00	22.46	165	SD	MET A 133	72.282	-3.590	-11.397	1.00	36.52
121	N	LVS A 128	72.080	-2.709	-1.336	1.00	25.87	166	CE	MET A 133	73.976	-3.108	-11.265	1.00	34.78
122	CA	LVS A 128	71.568	-1.383	-1.764	1.00	27.63	167	N	THR A 134	69.598	-1.070	-14.564	1.00	38.11
123	C	LVS A 128	72.616	-0.764	-2.712	1.00	27.55	168	CA	THR A 134	68.453	-1.786	-15.145	1.00	37.87
124	O	LVS A 128	73.804	-0.895	-2.438	1.00	24.66	169	C	THR A 134	69.034	-3.203	-15.229	1.00	38.03
125	CB	LVS A 128	71.296	-0.455	-0.592	1.00	26.80	170	O	THR A 134	70.166	-3.414	-15.685	1.00	35.72
126	CG	LVS A 128	70.839	0.946	-0.922	1.00	26.29	171	CB	THR A 134	67.747	-1.212	-16.162	1.00	39.56
127	CD	LVS A 128	69.376	1.128	-1.234	1.00	26.25	172	OG1	THR A 134	68.167	-1.836	-17.592	1.00	40.70
128	CE	LVS A 128	69.084	2.556	-1.653	1.00	27.49	173	CG2	THR A 134	67.867	0.296	-16.567	1.00	38.10
129	NZ	LVS A 128	69.797	3.575	-0.866	1.00	29.77	174	N	LEU A 135	68.277	-4.155	-14.682	1.00	38.56
130	N	LEU A 129	72.178	-0.105	-3.777	1.00	29.12	175	CA	LEU A 135	68.779	-5.531	-14.645	1.00	38.93

266	CA	THR A 148	89.108	-15.593	3.444	1.00	30.46	311	C	PRO A 154	77.070	-17.092	-8.125	1.00	29.11
267	C	THR A 148	89.841	-16.711	2.711	1.00	32.06	312	O	PRO A 154	76.389	-17.689	-7.291	1.00	28.76
268	O	THR A 148	91.043	-16.921	2.873	1.00	30.77	313	CB	PRO A 154	78.239	-18.829	-9.471	1.00	30.32
269	CB	THR A 148	88.182	-16.136	4.545	1.00	28.74	314	CG	PRO A 154	79.208	-19.853	-9.041	1.00	31.95
270	OG1	THR A 148	87.559	-15.026	5.205	1.00	25.09	315	CD	PRO A 154	79.709	-19.499	-7.665	1.00	30.13
271	CG2	THR A 148	88.854	-16.928	5.658	1.00	29.31	316	N	VAL A 155	76.635	-15.979	-8.687	1.00	29.63
272	N	THR A 149	89.131	-17.425	1.847	1.00	31.51	317	CA	VAL A 155	75.325	-15.376	-8.443	1.00	30.78
273	CA	THR A 149	89.650	-18.565	1.097	1.00	32.38	318	C	VAL A 155	74.378	-15.940	-9.509	1.00	30.85
274	C	THR A 149	90.032	-18.207	-0.336	1.00	34.28	319	O	VAL A 155	74.696	-15.745	-10.690	1.00	30.08
275	O	THR A 149	90.843	-18.860	-0.978	1.00	34.35	320	CB	VAL A 155	75.011	-13.871	-8.530	1.00	30.85
276	CB	THR A 149	88.573	-19.672	1.002	1.00	31.79	321	CG1	VAL A 155	73.695	-13.215	-8.115	1.00	20.00
277	OG1	THR A 149	87.433	-19.098	0.347	1.00	31.53	322	CG2	VAL A 155	76.117	-13.400	-7.604	1.00	29.33
278	CG2	THR A 149	88.174	-20.139	2.387	1.00	31.56	323	N	THR A 156	73.320	-16.648	-9.159	1.00	29.83
279	N	GLY A 150	89.415	-17.156	-0.867	1.00	34.70	324	CA	THR A 156	72.450	-17.270	-10.144	1.00	31.67
280	CA	GLY A 150	89.621	-16.692	-2.232	1.00	35.07	325	C	THR A 156	71.245	-16.427	-10.562	1.00	32.89
281	C	GLY A 150	88.528	-17.240	-3.148	1.00	34.60	326	O	THR A 156	70.632	-16.699	-11.621	1.00	32.33
282	O	GLY A 150	88.453	-16.846	-4.298	1.00	34.70	327	CB	THR A 156	71.956	-18.634	-9.635	1.00	31.70
283	N	GLU A 151	87.706	-18.163	-2.651	1.00	34.79	328	OG1	THR A 156	71.092	-18.419	-8.515	1.00	31.91
284	CA	GLU A 151	86.647	-18.768	-3.457	1.00	36.01	329	CG2	THR A 156	73.150	-19.479	-9.186	1.00	32.24
285	C	GLU A 151	85.618	-17.746	-3.946	1.00	35.57	330	N	SER A 157	70.880	-15.436	-9.730	1.00	31.06
286	O	GLU A 151	85.046	-16.957	-3.184	1.00	32.89	331	CA	SER A 157	69.833	-14.506	-10.141	1.00	30.56
287	CB	GLU A 151	85.878	-19.866	-2.699	1.00	36.86	332	C	SER A 157	69.803	-13.227	-9.308	1.00	29.60
288	CG	GLU A 151	84.457	-20.388	-2.912	1.00	39.81	333	O	SER A 157	70.337	-13.169	-8.195	1.00	27.35
289	CD	GLU A 151	83.800	-21.357	-1.955	1.00	41.00	334	CB	SER A 157	68.491	-15.222	-10.214	1.00	32.34
290	OE1	GLU A 151	83.941	-21.618	-0.761	1.00	20.00	335	OG	SER A 157	67.810	-15.173	-9.012	1.00	35.08
291	OE2	GLU A 151	82.953	-21.888	-2.659	1.00	20.00	336	N	ALA A 158	69.446	-12.117	-9.959	1.00	26.45
292	N	LYS A 152	85.373	-17.792	-5.258	1.00	34.10	337	CA	ALA A 158	69.453	-10.774	-9.423	1.00	27.24
293	CA	LYS A 152	84.388	-16.920	-5.880	1.00	33.14	338	C	ALA A 158	68.152	-10.053	-9.765	1.00	30.18
294	C	LYS A 152	83.100	-17.721	-5.895	1.00	32.88	339	O	ALA A 158	67.765	-9.918	-10.959	1.00	30.53
295	O	LYS A 152	83.174	-18.923	-6.156	1.00	34.46	340	CB	ALA A 158	70.645	-10.022	-9.985	1.00	26.36
296	CB	LYS A 152	84.713	-16.397	-7.291	1.00	33.96	341	N	VAL A 159	67.340	-9.812	-8.734	1.00	28.12
297	CG	LYS A 152	86.053	-15.890	-7.831	1.00	20.00	342	CA	VAL A 159	66.000	-9.269	-8.930	1.00	28.80
298	CD	LYS A 152	86.300	-15.397	-9.258	1.00	20.00	343	C	VAL A 159	65.789	-8.029	-8.074	1.00	28.52
299	CE	LYS A 152	87.720	-14.878	-9.009	1.00	20.00	344	O	VAL A 159	66.627	-7.709	-7.226	1.00	25.60
300	NZ	LYS A 152	88.820	-14.900	-9.971	1.00	20.00	345	CB	VAL A 159	64.846	-10.243	-8.667	1.00	29.04
301	N	ILE A 153	81.971	-17.105	-5.571	1.00	30.39	346	CG1	VAL A 159	64.965	-11.513	-9.494	1.00	29.16
302	CA	ILE A 153	80.697	-17.797	-5.515	1.00	30.18	347	CG2	VAL A 159	64.667	-10.636	-7.188	1.00	27.70
303	C	ILE A 153	79.726	-17.261	-6.561	1.00	30.58	348	N	SER A 160	64.643	-7.357	-8.283	1.00	28.60
304	O	ILE A 153	79.369	-16.087	-6.544	1.00	29.54	349	CA	SER A 160	63.738	-6.562	-6.141	1.00	27.31
305	CB	ILE A 153	80.079	-17.596	-4.102	1.00	30.99	350	C	SER A 160	64.422	-6.159	-7.460	1.00	27.56
306	CG1	ILE A 153	81.005	-18.163	-3.015	1.00	32.60	351	O	SER A 160	62.904	-7.468	-6.153	1.00	25.37
307	CG2	ILE A 153	78.708	-18.343	-4.058	1.00	30.51	352	CB	SER A 160	53.626	-5.076	-8.149	1.00	28.21
308	CD1	ILE A 153	80.665	-17.636	-1.620	1.00	33.71	353	OG	SER A 160	63.262	-4.072	-7.188	1.00	25.98
309	N	PRO A 154	79.304	-18.086	-7.516	1.00	30.89	354	N	ALA A 161	64.205	-5.955	-5.033	1.00	25.91
310	CA	PRO A 154	78.425	-17.617	-8.577	1.00	29.91	355	CA	ALA A 161	63.629	-6.241	-3.731	1.00	25.68

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356	C	ALA A 161	62.547	-5.238	-3.329	1.00 26.62	401	CA	LEU A 168	42.257	-5.482	-8.519	1.00 18.94
357	O	ALA A 161	61.886	-5.395	-2.296	1.00 23.95	402	C	LEU A 168	41.053	-4.647	-8.099	1.00 20.89
358	CB	ALA A 161	64.715	-6.344	-2.642	1.00 25.65	403	O	LEU A 168	40.431	-4.955	-7.048	1.00 21.09
359	N	ASN A 162	62.257	-4.216	-4.131	1.00 26.84	404	CB	LEU A 168	41.808	-6.925	-8.770	1.00 18.27
360	CA	ASN A 162	61.183	-3.278	-3.763	1.00 27.62	405	CG	LEU A 168	40.646	-7.136	-9.739	1.00 18.57
361	C	ASN A 162	59.841	-3.987	-3.818	1.00 28.07	406	CD1	LEU A 168	41.115	-6.720	-11.135	1.00 17.67
362	O	ASN A 162	59.547	-4.755	-4.741	1.00 28.17	407	CD2	LEU A 168	40.166	-8.607	-9.767	1.00 17.71
363	CB	ASN A 162	61.196	-2.092	-4.718	1.00 28.34	408	N	VAL A 169	40.726	-3.598	-8.865	1.00 20.18
364	CG	ASN A 162	62.395	-1.174	-4.643	1.00 29.74	409	CA	VAL A 169	39.571	-2.758	-8.519	1.00 19.68
365	OD1	ASN A 162	62.886	-0.911	-3.535	1.00 30.40	410	C	VAL A 169	38.501	-2.816	-9.592	1.00 20.02
366	ND2	ASN A 162	62.829	-0.625	-5.774	1.00 27.62	411	O	VAL A 169	38.871	-2.925	-10.765	1.00 19.91
367	N	PRO A 163	58.979	-3.767	-2.828	1.00 27.79	412	CB	VAL A 169	39.943	-1.260	-8.324	1.00 19.72
368	CA	PRO A 163	57.661	-4.372	-2.786	1.00 26.20	413	CG1	VAL A 169	40.903	-1.142	-7.131	1.00 17.22
369	C	PRO A 163	56.742	-3.804	-3.860	1.00 25.38	414	CG2	VAL A 169	40.600	-0.612	-9.541	1.00 18.93
370	O	PRO A 163	56.967	-2.735	-4.449	1.00 24.29	415	N	GLY A 170	37.224	-2.742	-9.246	1.00 18.55
371	CB	PRO A 163	57.181	-4.066	-1.369	1.00 27.88	416	CA	GLY A 170	36.172	-2.790	-10.248	1.00 18.73
372	CG	PRO A 163	57.870	-2.776	-1.027	1.00 28.89	417	C	GLY A 170	34.791	-3.031	-9.664	1.00 17.66
373	CD	PRO A 163	59.234	-2.875	-1.661	1.00 27.81	418	O	GLY A 170	34.639	-3.096	-8.438	1.00 17.25
374	N	VAL A 164	55.717	-4.569	-4.208	1.00 25.30	419	N	ASP A 171	33.806	-3.317	-10.500	1.00 18.35
375	CA	VAL A 164	54.721	-4.187	-5.220	1.00 25.51	420	CA	ASP A 171	32.470	-3.653	-10.006	1.00 22.28
376	C	VAL A 164	53.339	-4.283	-4.585	1.00 24.80	421	C	ASP A 171	32.356	-5.172	-9.771	1.00 22.87
377	O	VAL A 164	52.995	-5.340	-4.040	1.00 26.11	422	O	ASP A 171	31.275	-5.671	-9.490	1.00 21.75
378	CB	VAL A 164	54.802	-5.048	-6.493	1.00 24.71	423	CB	ASP A 171	31.304	-3.164	-10.866	1.00 22.13
379	CG1	VAL A 164	53.663	-4.752	-7.467	1.00 26.19	424	CG	ASP A 171	31.364	-3.728	-12.276	1.00 24.79
380	CG2	VAL A 164	56.125	-4.811	-7.253	1.00 25.42	425	OD1	ASP A 171	32.272	-4.532	-12.592	1.00 24.08
381	N	THR A 165	52.538	-3.233	-4.606	1.00 24.33	426	OD2	ASP A 171	30.463	-3.373	-13.068	1.00 25.44
382	CA	THR A 165	51.200	-3.270	-4.032	1.00 25.19	427	N	LEU A 172	33.459	-5.907	-9.824	1.00 23.38
383	C	THR A 165	50.176	-3.008	-5.166	1.00 24.41	428	CA	LEU A 172	33.556	-7.317	-9.519	1.00 23.45
384	O	THR A 165	49.956	-1.847	-5.503	1.00 21.40	429	C	LEU A 172	34.101	-7.426	-8.093	1.00 23.46
385	CB	THR A 165	50.966	-2.262	-2.897	1.00 26.83	430	O	LEU A 172	34.338	-8.531	-7.601	1.00 23.89
386	OG1	THR A 165	51.832	-2.523	-1.774	1.00 28.11	431	CB	LEU A 172	34.488	-8.066	-10.492	1.00 23.96
387	CG2	THR A 165	49.533	-2.347	-2.377	1.00 25.74	432	CG	LEU A 172	35.716	-7.388	-11.089	1.00 23.60
388	N	ALA A 166	49.546	-4.081	-5.643	1.00 22.25	433	CD1	LEU A 172	36.700	-6.874	-10.024	1.00 23.92
389	CA	ALA A 166	48.656	-3.909	-6.820	1.00 23.36	434	CD2	LEU A 172	36.501	-8.286	-12.049	1.00 22.64
390	C	ALA A 166	47.323	-4.512	-6.453	1.00 22.56	435	N	GLN A 173	34.427	-6.304	-7.425	1.00 22.02
391	O	ALA A 166	47.351	-5.703	-6.108	1.00 24.73	436	CA	GLN A 173	35.116	-6.409	-6.144	1.00 23.00
392	CB	ALA A 166	49.294	-4.589	-8.031	1.00 19.57	437	C	GLN A 173	34.301	-7.061	-5.012	1.00 25.30
393	N	VAL A 167	46.229	-3.768	-6.464	1.00 22.47	438	O	GLN A 173	34.956	-7.770	-4.222	1.00 23.45
394	CA	VAL A 167	44.939	-4.309	-6.043	1.00 19.46	439	CB	GLN A 173	35.715	-5.085	-5.640	1.00 19.82
395	C	VAL A 167	43.980	-4.333	-7.248	1.00 21.03	440	CG	GLN A 173	37.222	-5.133	-5.502	1.00 20.64
396	O	VAL A 167	43.901	-3.309	-7.917	1.00 18.72	441	CD	GLN A 173	37.865	-3.790	-5.190	1.00 20.89
397	CB	VAL A 167	44.310	-3.476	-4.911	1.00 20.70	442	OE1	GLN A 173	38.776	-3.712	-4.337	1.00 21.68
398	CG1	VAL A 167	42.832	-3.503	-4.525	1.00 18.70	443	NE2	GLN A 173	37.472	-2.762	-5.917	1.00 14.10
399	CG2	VAL A 167	45.155	-3.486	-3.651	1.00 22.11	444	N	GLN A 174	33.011	-6.766	-4.897	1.00 27.15
400	N	LEU A 168	43.264	-5.454	-7.447	1.00 19.41	445	CA	GLN A 174	32.211	-7.350	-3.808	1.00 30.17

446	C	GLN A 174	32.010	-8.853	-3.980	1.00 29.95	491	O	ASN A 181	34.253	0.299	-4.849	1.00 23.10
447	O	GLN A 174	32.162	-9.617	-3.030	1.00 29.74	492	CB	ASN A 181	32.221	-1.881	-6.393	1.00 24.36
448	CB	GLN A 174	30.806	-6.738	-3.686	1.00 30.31	493	CG	ASN A 181	31.526	-3.216	-6.503	1.00 23.81
449	CG	GLN A 174	30.791	-5.300	-3.184	1.00 31.02	494	OD1	ASN A 181	30.312	-3.231	-6.776	1.00 25.93
450	CD	GLN A 174	29.381	-4.727	-3.153	1.00 32.11	495	ND2	ASN A 181	32.208	-4.326	-6.339	1.00 19.94
451	OE1	GLN A 174	28.641	-4.750	-4.123	1.00 32.20	496	N	TRP A 182	35.132	-0.743	-6.657	1.00 23.37
452	NE2	GLN A 174	29.058	-4.103	-2.011	1.00 32.45	497	CA	TRP A 182	36.096	0.317	-6.986	1.00 22.89
453	N	ALA A 175	31.859	-9.290	-5.225	1.00 30.17	498	C	TRP A 182	36.812	0.884	-5.748	1.00 24.90
454	CA	ALA A 175	31.793	-10.722	-5.537	1.00 30.64	499	O	TRP A 182	36.686	2.061	-5.356	1.00 22.19
455	C	ALA A 175	33.072	-11.450	-5.174	1.00 30.81	500	CB	TRP A 182	35.440	1.390	-7.842	1.00 21.88
456	O	ALA A 175	33.044	-12.667	-4.926	1.00 31.59	501	CG	TRP A 182	34.968	0.888	-9.213	1.00 21.19
457	CB	ALA A 175	31.469	-10.864	-7.023	1.00 30.89	502	CD1	TRP A 182	33.661	0.662	-9.556	1.00 20.22
458	N	LEU A 176	34.188	-10.738	-5.050	1.00 29.83	503	CD2	TRP A 182	35.772	0.587	-10.354	1.00 20.33
459	CA	LEU A 176	35.474	-11.299	-4.683	1.00 30.69	504	NE1	TRP A 182	33.620	0.238	-10.890	1.00 21.14
460	C	LEU A 176	35.799	-11.058	-3.218	1.00 31.12	505	CE2	TRP A 182	34.899	0.206	-11.396	1.00 20.92
461	O	LEU A 176	36.912	-11.315	-2.771	1.00 31.07	506	CE3	TRP A 182	37.140	0.646	-10.652	1.00 19.83
462	CB	LEU A 176	36.587	-10.806	-5.622	1.00 30.20	507	C22	TRP A 182	35.335	-0.126	-12.679	1.00 19.37
463	CG	LEU A 176	36.490	-11.210	-7.098	1.00 30.54	508	C23	TRP A 182	37.588	0.290	-11.911	1.00 20.08
464	CD1	LEU A 176	37.534	-10.515	-7.971	1.00 28.99	509	CH2	TRP A 182	36.682	-0.111	-12.925	1.00 18.62
465	CD2	LEU A 176	36.726	-12.713	-7.263	1.00 30.40	510	N	SRP A 183	37.553	-0.028	-5.091	1.00 24.20
466	N	GLY A 177	34.829	-10.590	-2.432	1.00 33.38	511	CA	SRP A 183	38.166	0.298	-3.787	1.00 25.99
467	CA	GLY A 177	34.977	-10.426	-1.004	1.00 34.48	512	C	SRP A 183	39.619	-0.056	-3.755	1.00 25.00
468	C	GLY A 177	35.277	-9.040	-0.468	1.00 36.08	513	O	SRP A 183	40.038	-1.222	-3.552	1.00 27.68
469	O	GLY A 177	35.331	-8.865	0.764	1.00 35.24	514	CB	SRP A 183	37.250	-0.396	-2.744	1.00 27.72
470	N	ALA A 178	35.543	-8.079	-1.354	1.00 34.40	515	OG	SRP A 183	37.806	-0.303	-1.422	1.00 31.94
471	CA	ALA A 178	35.818	-6.733	-0.871	1.00 34.80	516	N	PRO A 184	40.504	0.901	-3.999	1.00 24.27
472	C	ALA A 178	34.509	-6.155	-0.321	1.00 33.76	517	CA	PRO A 184	41.936	0.660	-4.076	1.00 25.54
473	O	ALA A 178	33.439	-6.440	-0.842	1.00 33.43	518	C	PRO A 184	42.583	0.218	-2.771	1.00 27.63
474	CB	ALA A 178	36.359	-5.829	-1.970	1.00 32.96	519	O	PRO A 184	43.702	-0.312	-2.819	1.00 26.74
475	N	ALA A 179	34.601	-5.282	0.670	1.00 33.57	520	CB	PRO A 184	42.567	2.002	-4.480	1.00 25.19
476	CA	ALA A 179	33.434	-4.614	1.223	1.00 32.22	521	CG	PRO A 184	41.436	2.850	-4.939	1.00 27.00
477	C	ALA A 179	32.707	-3.731	0.213	1.00 30.62	522	CD	PRO A 184	40.171	2.317	-4.293	1.00 25.48
478	O	ALA A 179	31.466	-3.697	0.192	1.00 30.86	523	N	ASP A 185	41.953	0.501	-1.660	1.00 28.67
479	CB	ALA A 179	33.856	-3.733	2.401	1.00 34.25	524	CA	ASP A 185	42.469	0.243	-0.330	1.00 35.01
480	N	ASN A 180	33.420	-2.907	-0.561	1.00 29.04	525	C	ASP A 185	42.168	-1.154	0.186	1.00 32.77
481	CA	ASN A 180	32.851	-2.015	-1.558	1.00 28.58	526	O	ASP A 185	42.631	-1.481	1.276	1.00 32.78
482	C	ASN A 180	33.499	-2.211	-2.939	1.00 27.39	527	CB	ASP A 185	41.794	1.331	0.575	1.00 40.72
483	O	ASN A 180	34.638	-2.689	-3.042	1.00 26.95	528	CG	ASP A 185	40.328	0.971	0.823	1.00 45.75
484	CB	ASN A 180	32.957	-0.521	-1.148	1.00 29.90	529	OD1	ASP A 185	39.796	-0.145	0.631	1.00 49.67
485	CG	ASN A 180	32.103	-0.258	0.104	1.00 31.68	530	OD2	ASP A 185	39.665	1.968	1.250	1.00 48.92
486	OD1	ASN A 180	30.885	-0.552	0.100	1.00 34.34	531	N	ASP A 186	41.216	-1.836	-0.471	1.00 30.11
487	ND2	ASN A 180	32.750	0.063	1.209	1.00 32.41	532	CA	ASP A 186	40.727	-3.109	0.072	1.00 29.50
488	N	ASN A 181	32.825	-1.852	-4.017	1.00 25.75	533	C	ASP A 186	41.595	-4.279	-0.355	1.00 28.84
489	CA	ASN A 181	33.370	-1.875	-5.372	1.00 25.22	534	O	ASP A 186	41.578	-4.767	-1.473	1.00 26.82
490	C	ASN A 181	34.287	-0.603	-5.625	1.00 24.74	535	CB	ASP A 186	39.253	-3.271	-0.280	1.00 29.89

536	CG	ASP	A	186	38.521	-4.309	0.548	1.00	30.33	581	CA	LVS	A	192	50.006	-12.052	-4.827	1.00	24.86
537	OD1	ASP	A	186	39.135	-5.357	0.847	1.00	30.32	582	C	LVS	A	192	51.232	-12.227	-5.700	1.00	26.50
538	OD2	ASP	A	186	37.337	-4.120	0.897	1.00	29.44	583	O	LVS	A	192	51.100	-12.428	-6.912	1.00	26.86
539	N	ASP	A	187	42.390	-4.757	0.617	1.00	28.04	584	CB	LVS	A	192	49.560	-13.491	-4.421	1.00	25.31
540	CA	ASP	A	187	43.314	-5.849	0.376	1.00	28.05	585	CG	LVS	A	192	48.449	-13.455	-3.375	1.00	27.13
541	C	ASP	A	187	42.680	-7.218	0.204	1.00	26.64	586	CD	LVS	A	192	47.815	-14.750	-3.079	0.00	20.00
542	O	ASP	A	187	43.469	-8.146	0.051	1.00	26.92	587	CE	LVS	A	192	46.420	-14.700	-2.448	0.00	20.00
543	CB	ASP	A	187	44.447	-5.977	1.403	1.00	29.12	588	NZ	LVS	A	192	46.039	-16.034	-1.988	0.00	20.00
544	CG	ASP	A	187	45.562	-5.006	1.075	1.00	29.66	589	N	LVS	A	193	52.413	-12.326	-5.098	1.00	27.68
545	OD1	ASP	A	187	45.560	-4.414	-0.035	1.00	29.31	590	CA	LVS	A	193	53.593	-12.532	-5.943	1.00	32.22
546	OD2	ASP	A	187	46.419	-4.719	1.940	1.00	30.32	591	C	LVS	A	193	53.825	-13.987	-6.288	1.00	32.50
547	N	HIS	A	188	41.382	-7.380	0.101	1.00	25.81	592	O	LVS	A	193	53.939	-14.822	-5.409	1.00	30.76
548	CA	HIS	A	188	40.750	-8.635	-0.234	1.00	28.57	593	CB	LVS	A	193	54.734	-11.805	-5.260	1.00	35.25
549	C	HIS	A	188	41.034	-8.980	-1.719	1.00	28.04	594	CG	LVS	A	193	56.021	-12.513	-4.979	1.00	39.64
550	O	HIS	A	188	40.988	-10.162	-2.051	1.00	25.11	595	CD	LVS	A	193	57.217	-11.595	-5.033	1.00	41.28
551	CB	HIS	A	188	39.247	-8.622	0.001	1.00	31.30	596	CE	LVS	A	193	58.106	-11.653	-3.808	1.00	44.51
552	CG	HIS	A	188	38.773	-8.598	1.420	1.00	35.25	597	NZ	LVS	A	193	59.154	-10.583	-3.791	1.00	45.93
553	ND1	HIS	A	188	38.178	-9.695	2.019	1.00	36.56	598	N	ILE	A	194	53.836	-14.305	-7.593	1.00	30.97
554	CD2	HIS	A	188	38.785	-7.621	2.366	1.00	36.05	599	CA	ILE	A	194	54.161	-15.631	-8.117	1.00	29.28
555	CE1	HIS	A	188	37.843	-9.392	3.263	1.00	37.12	600	C	ILE	A	194	55.654	-15.716	-8.412	1.00	28.94
556	NE2	HIS	A	188	38.209	-8.137	3.496	1.00	38.08	601	O	ILE	A	194	56.334	-16.725	-8.177	1.00	28.26
557	N	THR	A	189	41.419	-8.003	-2.549	1.00	25.78	602	CB	ILE	A	194	53.341	-15.917	-9.394	1.00	30.80
558	CA	THR	A	189	41.749	-8.277	-3.944	1.00	25.63	603	CG1	ILE	A	194	51.872	-15.560	-9.172	1.00	29.46
559	C	THR	A	189	43.164	-7.831	-4.295	1.00	26.53	604	CD2	ILE	A	194	53.505	-17.363	-9.869	1.00	30.31
560	O	THR	A	189	43.525	-7.508	-5.446	1.00	25.53	605	CG1	ILE	A	194	51.129	-16.279	-8.076	1.00	29.66
561	CB	THR	A	189	40.736	-7.696	-4.945	1.00	24.83	606	N	ASN	A	195	56.246	-14.658	-8.969	1.00	26.41
562	CG1	THR	A	189	40.551	-6.312	-4.648	1.00	23.22	607	CA	ASN	A	195	57.689	-14.582	-9.209	1.00	25.15
563	CG2	THR	A	189	39.397	-8.428	-4.913	1.00	24.10	608	C	ASN	A	195	57.982	-13.108	-9.056	1.00	25.32
564	N	LEU	A	190	44.036	-7.871	-3.278	1.00	24.47	609	O	ASN	A	195	57.060	-12.285	-9.010	1.00	24.84
565	CA	LEU	A	190	45.446	-7.592	-3.497	1.00	25.02	610	CB	ASN	A	195	58.205	-15.255	-10.468	1.00	26.01
566	C	LEU	A	190	46.106	-8.740	-4.276	1.00	24.54	611	CG	ASN	A	195	58.002	-14.588	-11.816	1.00	23.49
567	O	LEU	A	190	45.947	-9.871	-3.821	1.00	24.54	612	OD1	ASN	A	195	58.324	-13.419	-11.979	1.00	22.62
568	CB	LEU	A	190	46.115	-7.493	-2.126	1.00	25.49	613	ND2	ASN	A	195	57.463	-15.271	-12.821	1.00	21.61
569	CG	LEU	A	190	47.612	-7.221	-2.066	1.00	26.63	614	N	PRO	A	196	59.222	-12.681	-8.921	1.00	27.18
570	CD1	LEU	A	190	47.961	-5.811	-2.561	1.00	26.87	615	CA	PRO	A	196	59.566	-11.282	-8.695	1.00	27.81
571	CD2	LEU	A	190	48.107	-7.483	-0.649	1.00	26.92	616	C	PRO	A	196	59.014	-10.304	-9.712	1.00	28.82
572	N	LEU	A	191	46.785	-8.501	-5.397	1.00	23.25	617	O	PRO	A	196	58.874	-9.118	-9.403	1.00	29.64
573	CA	LEU	A	191	47.424	-9.589	-6.120	1.00	22.73	618	CB	PRO	A	196	61.088	-11.245	-8.660	1.00	27.55
574	C	LEU	A	191	48.627	-10.118	-5.353	1.00	23.41	619	CG	PRO	A	196	61.562	-12.641	-8.735	1.00	27.99
575	O	LEU	A	191	49.390	-9.351	-4.748	1.00	21.57	620	CD	PRO	A	196	60.400	-13.571	-8.910	1.00	27.24
576	CB	LEU	A	191	47.921	-9.125	-7.510	1.00	21.62	621	N	ASN	A	197	58.728	-10.737	-10.939	1.00	28.40
577	CG	LEU	A	191	46.880	-8.960	-8.614	1.00	21.93	622	CA	ASN	A	197	58.152	-9.868	-11.964	1.00	27.61
578	CD1	LEU	A	191	45.698	-8.077	-8.268	1.00	18.64	623	C	ASN	A	197	56.808	-10.412	-12.426	1.00	26.54
579	CD2	LEU	A	191	47.599	-8.457	-9.886	1.00	21.63	624	O	ASN	A	197	56.446	-10.216	-13.588	1.00	24.74
580	N	LVS	A	192	48.898	-11.403	-5.497	1.00	23.59	625	CB	ASN	A	197	59.156	-9.685	-13.114	1.00	25.82

626	CG	ASN	A	197	58.874	-8.553	-14.073	1.00	24.90	671	OG	SRK	A	202	43.669	-17.342	-10.101	1.00	24.55
627	OD1	ASN	A	197	58.401	-7.487	-13.679	1.00	25.87	672	N	GLY	A	203	39.768	-15.823	-8.623	1.00	24.80
628	ND2	ASN	A	197	59.143	-8.694	-15.374	1.00	22.51	673	CA	GLY	A	203	38.565	-15.892	-7.834	1.00	25.89
629	N	LSU	A	198	56.003	-11.008	-11.527	1.00	25.03	674	C	GLY	A	203	37.359	-16.159	-8.711	1.00	28.12
630	CA	LSU	A	198	54.709	-11.567	-11.921	1.00	25.50	675	O	GLY	A	203	37.385	-15.914	-9.919	1.00	28.11
631	C	LSU	A	198	53.734	-11.604	-10.757	1.00	24.75	676	N	THR	A	204	36.305	-16.716	-8.088	1.00	27.74
632	O	LSU	A	198	54.037	-12.353	-9.805	1.00	24.83	677	CA	THR	A	204	35.097	-17.110	-8.779	1.00	26.86
633	CB	LSU	A	198	54.639	-12.947	-12.600	1.00	26.19	678	C	THR	A	204	34.105	-15.971	-8.927	1.00	26.50
634	CG	LSU	A	198	53.385	-13.711	-13.032	1.00	29.17	679	O	THR	A	204	33.813	-15.312	-7.936	1.00	26.91
635	CD1	LSU	A	198	52.653	-13.174	-14.263	1.00	28.46	680	CB	THR	A	204	34.383	-18.207	-7.933	1.00	29.21
636	CD2	LSU	A	198	54.064	-15.009	-13.469	1.00	31.33	681	OG1	THR	A	204	35.262	-19.322	-7.816	1.00	28.46
637	N	TYR	A	199	52.635	-10.883	-10.781	1.00	22.56	682	CG2	THR	A	204	33.059	-18.617	-8.581	1.00	28.38
638	CA	TYR	A	199	51.640	-10.795	-9.724	1.00	22.64	683	N	LSU	A	205	33.575	-15.738	-10.119	1.00	25.28
639	C	TYR	A	199	50.281	-11.272	-10.192	1.00	23.37	684	CA	LSU	A	205	32.594	-14.705	-10.324	1.00	27.14
640	O	TYR	A	199	49.898	-10.900	-11.326	1.00	21.85	685	C	LSU	A	205	31.303	-15.289	-10.898	1.00	29.05
641	CB	TYR	A	199	51.488	-9.332	-9.172	1.00	22.41	686	O	LSU	A	205	31.325	-16.121	-11.802	1.00	27.54
642	CG	TYR	A	199	52.673	-9.037	-8.251	1.00	24.19	687	CB	LSU	A	205	33.139	-13.666	-11.307	1.00	27.39
643	CD1	TYR	A	199	52.525	-9.019	-6.870	1.00	24.33	688	CG	LSU	A	205	34.340	-12.803	-10.896	1.00	27.95
644	CD2	TYR	A	199	53.955	-8.856	-7.753	1.00	24.63	689	CD1	LSU	A	205	34.858	-12.022	-12.101	1.00	27.28
645	CE1	TYR	A	199	53.599	-8.782	-6.021	1.00	23.22	690	CD2	LSU	A	205	33.999	-11.861	-9.743	1.00	29.19
646	CE2	TYR	A	199	55.407	-8.650	-7.934	1.00	24.30	691	N	PRO	A	206	30.154	-14.795	-10.441	1.00	30.40
647	CZ	TYR	A	199	54.848	-8.607	-6.552	1.00	25.35	692	CA	PRO	A	206	28.870	-15.199	-11.005	1.00	30.93
648	OH	TYR	A	199	55.967	-8.424	-5.737	1.00	25.36	693	C	PRO	A	206	28.882	-14.794	-12.473	1.00	31.99
649	N	GLN	A	200	49.593	-12.153	-9.437	1.00	21.46	694	O	PRO	A	206	29.702	-13.916	-12.809	1.00	32.25
650	CA	GLN	A	200	48.319	-12.703	-9.851	1.00	22.78	695	CB	PRO	A	206	27.830	-14.370	-10.241	1.00	30.06
651	C	GLN	A	200	47.308	-12.901	-8.709	1.00	23.92	696	CG	PRO	A	206	28.518	-13.896	-9.020	1.00	30.95
652	O	GLN	A	200	47.642	-12.965	-7.529	1.00	23.20	697	CD	PRO	A	206	30.006	-13.818	-9.345	1.00	31.23
653	CB	GLN	A	200	48.460	-14.071	-10.554	1.00	23.72	698	N	ALA	A	207	27.959	-15.236	-13.292	1.00	30.94
654	CG	GLN	A	200	49.326	-14.123	-11.818	1.00	23.30	699	CA	ALA	A	207	27.829	-14.752	-14.647	1.00	32.79
655	CD	GLN	A	200	49.357	-15.468	-12.509	1.00	24.08	700	C	ALA	A	207	27.525	-13.250	-14.646	1.00	33.93
656	OEL	GLN	A	200	48.907	-15.563	-13.665	1.00	25.79	701	O	ALA	A	207	26.875	-12.784	-13.698	1.00	33.84
657	NE2	GLN	A	200	49.802	-16.529	-11.838	1.00	21.68	702	CB	ALA	A	207	26.644	-15.405	-15.344	1.00	33.37
658	N	LEU	A	201	46.029	-12.854	-9.068	1.00	22.79	703	N	GLY	A	208	27.891	-12.554	-15.717	1.00	33.30
659	CA	LEU	A	201	44.878	-13.063	-8.223	1.00	23.86	704	CA	GLY	A	208	27.627	-11.117	-15.815	1.00	33.40
660	C	LEU	A	201	43.871	-13.926	-8.993	1.00	22.76	705	C	GLY	A	208	28.764	-10.431	-16.590	1.00	34.81
661	O	LEU	A	201	43.615	-13.595	-10.149	1.00	20.39	706	O	GLY	A	208	29.748	-11.089	-16.954	1.00	34.75
662	CB	LEU	A	201	44.180	-11.770	-7.798	1.00	24.31	707	N	THR	A	209	28.631	-9.147	-16.855	1.00	33.68
663	CG	LEU	A	201	42.984	-11.871	-6.855	1.00	27.82	708	CA	THR	A	209	29.649	-8.364	-17.553	1.00	35.01
664	CD1	LEU	A	201	43.423	-12.292	-5.451	1.00	28.00	709	C	THR	A	209	30.168	-7.337	-16.549	1.00	32.85
665	CD2	LEU	A	201	42.247	-10.531	-6.725	1.00	26.81	710	O	THR	A	209	29.371	-6.687	-15.843	1.00	31.81
666	N	SER	A	202	43.269	-14.938	-8.367	1.00	21.06	711	CB	THR	A	209	29.126	-7.714	-18.837	1.00	37.54
667	CA	SER	A	202	42.217	-15.727	-8.956	1.00	20.94	712	OG1	THR	A	209	30.036	-6.711	-19.353	1.00	40.79
668	C	SER	A	202	40.969	-15.724	-8.085	1.00	24.18	713	CG2	THR	A	209	27.808	-7.044	-18.521	1.00	38.82
669	O	SER	A	202	41.140	-15.747	-6.843	1.00	26.01	714	N	TYR	A	210	31.475	-7.356	-16.327	1.00	28.47
670	CB	SER	A	202	42.700	-17.198	-9.057	1.00	21.57	715	CA	TYR	A	210	32.119	-6.499	-15.331	1.00	25.61

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716	C	TYR A 210	33.148	-5.574	-15.968	1.00 23.20	761	CG1 ILE A 214	45.679	-4.554	-12.610	1.00 20.30
717	O	TYR A 210	33.511	-5.730	-17.129	1.00 20.43	762	CG2 ILE A 214	46.957	-3.514	-10.703	1.00 18.99
718	CB	TYR A 210	32.853	-7.361	-14.285	1.00 25.13	763	CD1 ILE A 214	44.772	-5.587	-11.986	1.00 19.54
719	CG	TYR A 210	32.043	-8.437	-13.604	1.00 25.77	764	N ALA A 215	44.970	-0.894	-9.489	1.00 21.29
720	CD1	TYR A 210	31.418	-8.187	-12.385	1.00 26.19	765	CA ALA A 215	45.406	0.360	-8.837	1.00 21.91
721	CD2	TYR A 210	31.878	-9.699	-14.159	1.00 26.65	766	C ALA A 215	46.590	0.082	-7.923	1.00 22.37
722	CE1	TYR A 210	30.647	-9.141	-11.755	1.00 25.94	767	O ALA A 215	46.588	-0.953	-7.226	1.00 21.58
723	CE2	TYR A 210	31.129	-10.686	-13.531	1.00 26.59	768	CB ALA A 215	44.222	0.911	-7.989	1.00 20.97
724	CZ	TYR A 210	30.508	-10.392	-12.330	1.00 27.30	769	N LEU A 216	47.641	0.873	-7.988	1.00 21.99
725	OH	TYR A 210	29.776	-11.352	-11.675	1.00 28.27	770	CA LEU A 216	48.845	0.752	-7.159	1.00 22.55
726	N	GLN A 211	33.707	-4.664	-15.180	1.00 21.51	771	C LEU A 216	48.759	1.510	-5.817	1.00 24.71
727	CA	GLN A 211	34.770	-3.769	-15.611	1.00 21.91	772	O LEU A 216	48.006	2.458	-5.641	1.00 22.08
728	C	GLN A 211	35.851	-3.700	-14.517	1.00 20.11	773	CB LEU A 216	50.029	1.290	-7.964	1.00 23.76
729	O	GLN A 211	35.444	-3.737	-13.367	1.00 19.22	774	CG LEU A 216	51.686	0.786	-9.825	1.00 22.16
730	CB	GLN A 211	34.270	-2.358	-15.949	1.00 20.26	775	CD1 LEU A 216	50.319	0.462	-9.216	1.00 22.14
731	CG	GLN A 211	33.515	-2.252	-17.274	1.00 21.03	776	CD2 LEU A 216	50.316	-1.042	-8.946	1.00 24.20
732	CD	GLN A 211	32.948	-0.889	-17.595	1.00 21.84	777	N ASP A 217	49.548	1.000	-4.839	1.00 24.74
733	OE1	GLN A 211	32.192	-0.698	-18.590	1.00 23.95	778	CA ASP A 217	49.861	1.748	-3.610	1.00 28.00
734	NE2	GLN A 211	33.387	0.136	-16.876	1.00 20.75	779	C ASP A 217	48.639	2.264	-2.839	1.00 29.70
735	N	TYR A 212	37.144	-3.613	-14.861	1.00 18.80	780	O ASP A 217	48.678	3.296	-2.182	1.00 30.51
736	CA	TYR A 212	38.126	-3.616	-13.782	1.00 19.43	781	CB ASP A 217	50.783	2.907	-3.980	1.00 27.70
737	C	TYR A 212	39.418	-2.932	-14.206	1.00 20.03	782	CG ASP A 217	52.039	2.351	-4.632	1.00 28.23
738	O	TYR A 212	39.722	-2.780	-15.384	1.00 17.17	783	OD1 ASP A 217	52.497	1.300	-4.187	1.00 25.51
739	CB	TYR A 212	38.434	-5.067	-13.433	1.00 20.14	784	OD2 ASP A 217	52.537	2.962	-5.574	1.00 29.46
740	CG	TYR A 212	39.327	-5.644	-14.475	1.00 20.47	785	N HIS A 218	47.515	1.528	-2.878	1.00 28.93
741	CD1	TYR A 212	38.790	-6.478	-15.451	1.00 19.52	786	CA HIS A 218	46.336	1.913	-2.179	1.00 31.04
742	CD2	TYR A 212	40.715	-5.503	-14.382	1.00 19.82	787	C HIS A 218	45.820	3.308	-2.512	1.00 32.01
743	CE1	TYR A 212	39.622	-7.192	-16.297	1.00 18.82	788	O HIS A 218	45.314	3.968	-1.594	1.00 33.76
744	CE2	TYR A 212	41.549	-6.216	-15.233	1.00 20.89	789	CB HIS A 218	46.580	1.848	-0.656	1.00 32.62
745	CZ	TYR A 212	41.006	-7.061	-16.184	1.00 19.83	790	CG HIS A 218	46.763	0.494	-0.095	1.00 34.70
746	OH	TYR A 212	41.824	-7.773	-17.038	1.00 20.51	791	ND1 HIS A 218	46.289	-0.669	-0.712	1.00 35.05
747	N	LYS A 213	40.166	-2.472	-13.189	1.00 18.54	792	CD2 HIS A 218	47.351	0.031	1.035	1.00 36.61
748	CA	LYS A 213	41.504	-1.960	-13.442	1.00 19.62	793	CE1 HIS A 218	46.572	-1.745	-0.006	1.00 35.70
749	C	LYS A 213	42.481	-2.457	-12.374	1.00 19.10	794	NE2 HIS A 218	47.230	-1.346	1.068	1.00 38.00
750	O	LYS A 213	42.131	-3.179	-11.451	1.00 21.19	795	N SER A 219	45.873	3.742	-3.746	1.00 30.50
751	CB	LYS A 213	41.449	-0.429	-13.444	1.00 20.40	796	CA SER A 219	45.437	5.088	-4.114	1.00 29.81
752	CG	LYS A 213	40.902	0.131	-14.757	1.00 19.33	797	C SER A 219	44.927	5.097	-5.553	1.00 28.38
753	CD	LYS A 213	41.325	1.584	-14.995	1.00 21.89	798	O SER A 219	45.236	4.171	-6.317	1.00 26.48
754	CE	LYS A 213	40.838	2.532	-13.895	1.00 24.44	799	CB SER A 219	46.673	5.978	-3.940	1.00 31.74
755	NZ	LYS A 213	41.231	3.905	-14.220	1.00 26.58	800	OG SER A 219	46.686	7.146	-4.725	1.00 33.53
756	N	ILE A 214	43.762	-2.212	-12.362	1.00 18.54	801	N TRP A 220	44.295	6.201	-5.943	1.00 26.47
757	CA	ILE A 214	44.727	-2.502	-11.342	1.00 19.13	802	CA TRP A 220	43.880	6.481	-7.293	1.00 27.86
758	C	ILE A 214	45.225	-1.142	-10.779	1.00 20.65	803	C TRP A 220	44.969	7.170	-8.118	1.00 28.10
759	O	ILE A 214	45.930	-0.422	-11.489	1.00 17.06	804	O TRP A 220	44.749	7.371	-9.326	1.00 27.08
760	CB	ILE A 214	45.969	-3.255	-11.847	1.00 19.87	805	CB TRP A 220	42.620	7.353	-7.351	1.00 28.03

806	CG	TRP A 220	41.346	6.631	-7.044	1.00	27.68	851	O	PRO A 225	44.313	2.161	-16.872	1.00	21.99
807	CD1	TRP A 220	40.441	6.925	-6.071	1.00	26.78	852	CB	PRO A 225	45.385	-0.335	-19.294	1.00	23.11
808	CD2	TRP A 220	40.843	5.467	-7.730	1.00	26.84	853	CG	PRO A 225	44.382	-1.484	-19.173	1.00	23.73
809	NE1	TRP A 220	39.395	6.022	-6.110	1.00	27.04	854	CD	PRO A 225	43.979	-1.435	-17.622	1.00	22.80
810	CE2	TRP A 220	39.632	5.109	-7.121	1.00	26.56	855	N	GLY A 226	45.077	2.458	-19.001	1.00	21.76
811	CE3	TRP A 220	41.320	4.690	-8.788	1.00	27.09	856	CA	GLY A 226	44.559	3.812	-19.040	1.00	21.93
812	C22	TRP A 220	38.876	4.018	-7.520	1.00	25.18	857	C	GLY A 226	43.022	3.923	-19.125	1.00	23.76
813	C23	TRP A 220	40.583	3.615	-9.210	1.00	26.81	858	O	GLY A 226	42.405	4.932	-18.809	1.00	23.80
814	CH2	TRP A 220	39.369	3.287	-8.557	1.00	26.52	859	N	ASN A 227	42.466	2.802	-19.616	1.00	24.79
815	N	ASN A 221	46.109	7.509	-7.535	1.00	27.91	860	CA	ASN A 227	41.018	2.737	-19.670	1.00	24.79
816	CA	ASN A 221	47.167	8.184	-8.277	1.00	29.33	861	C	ASN A 227	40.364	1.416	-18.959	1.00	23.66
817	C	ASN A 221	47.613	7.441	-9.528	1.00	29.98	862	O	ASN A 227	41.160	0.489	-18.779	1.00	21.15
818	O	ASN A 221	47.834	8.056	-10.580	1.00	29.96	863	CB	ASN A 227	40.210	2.594	-21.106	1.00	26.98
819	CB	ASN A 221	48.384	8.377	-7.354	1.00	32.21	864	CG	ASN A 227	40.485	3.892	-21.877	1.00	29.55
820	CG	ASN A 221	48.207	9.429	-6.270	1.00	35.96	865	OD1	ASN A 227	40.418	4.994	-21.332	1.00	31.48
821	OD1	ASN A 221	47.216	10.178	-6.276	1.00	39.36	866	ND2	ASN A 227	40.823	3.724	-23.148	1.00	31.22
822	ND2	ASN A 221	49.141	9.546	-5.324	1.00	35.91	867	N	ASN A 228	39.094	1.377	-18.571	1.00	23.20
823	N	THR A 222	47.864	6.135	-9.421	1.00	28.62	868	CA	ASN A 228	38.573	0.197	-17.841	1.00	22.62
824	CA	THR A 222	48.373	5.326	-10.511	1.00	27.05	869	C	ASN A 228	38.683	-1.049	-18.724	1.00	22.14
825	C	THR A 222	47.570	4.034	-10.661	1.00	25.67	870	O	ASN A 228	38.483	-0.972	-19.949	1.00	21.31
826	O	THR A 222	47.542	3.226	-9.734	1.00	22.27	871	CB	ASN A 228	37.100	0.435	-17.487	1.00	21.69
827	CB	THR A 222	49.869	5.008	-10.320	1.00	28.65	872	CG	ASN A 228	36.803	1.486	-16.423	1.00	21.12
828	CG1	THR A 222	50.605	6.252	-10.393	1.00	30.47	873	OD1	ASN A 228	35.598	1.769	-16.125	1.00	21.53
829	CG2	THR A 222	50.488	4.129	-11.413	1.00	28.53	874	ND2	ASN A 228	37.794	2.076	-15.831	1.00	18.06
830	N	SER A 223	47.016	3.848	-11.867	1.00	23.93	875	N	VAL A 229	38.857	-2.232	-18.162	1.00	22.54
831	CA	SER A 223	46.277	2.629	-12.199	1.00	22.41	876	CA	VAL A 229	38.894	-3.464	-18.981	1.00	20.80
832	C	SER A 223	46.504	2.179	-13.656	1.00	22.11	877	O	VAL A 229	37.524	-4.125	-18.851	1.00	20.25
833	O	SER A 223	46.870	3.009	-14.521	1.00	20.61	878	C	VAL A 229	37.078	-4.359	-17.734	1.00	20.94
834	CB	SER A 223	44.791	2.770	-11.925	1.00	21.37	879	CB	VAL A 229	39.990	-4.473	-18.584	1.00	19.95
835	OG	SER A 223	44.098	3.680	-12.748	1.00	21.13	880	CG1	VAL A 229	39.902	-5.771	-19.415	1.00	14.74
836	N	TYR A 224	46.306	0.904	-13.924	1.00	19.54	881	CG2	VAL A 229	41.389	-3.855	-18.689	1.00	15.89
837	CA	TYR A 224	46.392	0.447	-15.308	1.00	20.33	882	N	SER A 230	36.894	-4.469	-19.964	1.00	21.31
838	C	TYR A 224	45.256	-0.515	-15.656	1.00	23.40	883	CA	SER A 230	35.595	-5.158	-19.969	1.00	22.94
839	O	TYR A 224	44.678	-1.178	-14.806	1.00	21.40	884	C	SER A 230	35.778	-6.674	-19.896	1.00	24.31
840	CB	TYR A 224	47.730	-0.269	-15.496	1.00	20.56	885	O	SER A 230	36.593	-7.269	-20.616	1.00	21.95
841	CG	TYR A 224	48.851	0.617	-15.090	1.00	20.58	886	CB	SER A 230	34.819	-4.769	-21.221	1.00	24.67
842	CD1	TYR A 224	49.428	0.464	-13.833	1.00	21.98	887	OG	SER A 230	33.548	-5.431	-21.269	1.00	28.19
843	CD2	TYR A 224	49.429	1.488	-16.013	1.00	22.63	888	N	LEU A 231	35.049	-7.328	-18.993	1.00	24.99
844	CE1	TYR A 224	50.582	1.159	-13.505	1.00	22.51	889	CA	LEU A 231	35.108	-8.754	-18.760	1.00	26.33
845	CE2	TYR A 224	50.582	2.166	-15.685	1.00	23.45	890	C	LEU A 231	33.709	-9.391	-18.724	1.00	29.37
846	C2	TYR A 224	51.161	2.018	-14.440	1.00	26.98	891	O	LEU A 231	32.966	-9.135	-17.764	1.00	28.67
847	OH	TYR A 224	52.340	2.665	-14.126	1.00	23.73	892	CB	LEU A 231	35.779	-9.047	-17.422	1.00	25.50
848	N	PRO A 225	44.910	-0.545	-16.957	1.00	23.50	893	CG	LEU A 231	35.801	-10.449	-16.823	1.00	26.01
849	CA	PRO A 225	45.501	0.350	-17.935	1.00	22.64	894	CD1	LEU A 231	36.671	-11.424	17.607	1.00	25.54
850	C	PRO A 225	44.900	1.756	-17.867	1.00	22.45	895	CD2	LEU A 231	36.348	-10.425	-15.384	1.00	25.86

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2426	N	PRO A 430	44.223	-8.379	38.259	1.00 17.36	2471	CD1	ILE A 435	49.227	-1.169	38.568	1.00 13.44
2427	CA	PRO A 430	44.798	-7.059	38.201	1.00 17.36	2472	N	TYR A 436	51.082	2.759	42.563	1.00 13.59
2428	C	PRO A 430	43.884	-5.954	38.671	1.00 16.98	2473	CA	TYR A 436	51.698	4.037	42.855	1.00 15.25
2429	O	PRO A 430	44.439	-4.967	39.171	1.00 15.58	2474	C	TYR A 436	53.109	4.093	42.264	1.00 15.01
2430	CB	PRO A 430	45.274	-6.889	36.756	1.00 17.72	2475	O	TYR A 436	53.988	3.279	42.617	1.00 14.02
2431	CG	PRO A 430	45.459	-8.315	36.305	1.00 17.97	2476	CB	TYR A 436	51.711	4.156	44.367	1.00 15.16
2432	CD	PRO A 430	44.377	-9.110	36.977	1.00 16.77	2477	CG	TYR A 436	52.196	5.355	45.116	1.00 16.16
2433	N	VAL A 431	42.554	-5.999	38.575	1.00 16.17	2478	CD1	TYR A 436	51.289	6.303	45.576	1.00 15.41
2434	CA	VAL A 431	41.696	-4.882	39.029	1.00 14.93	2479	CD2	TYR A 436	53.549	5.498	45.460	1.00 15.75
2435	C	VAL A 431	41.724	-4.718	40.549	1.00 16.96	2480	CB1	TYR A 436	51.717	7.384	46.327	1.00 16.02
2436	O	VAL A 431	41.207	-3.711	41.066	1.00 14.24	2481	CB2	TYR A 436	53.987	6.584	46.218	1.00 15.63
2437	CB	VAL A 431	40.236	-5.000	38.552	1.00 14.61	2482	C2	TYR A 436	53.058	7.496	46.674	1.00 15.39
2438	CG1	VAL A 431	40.141	-5.164	37.018	1.00 11.37	2483	OH	TYR A 436	53.434	8.562	47.464	1.00 16.13
2439	CG2	VAL A 431	39.470	-6.174	39.204	1.00 9.63	2484	N	GLU A 437	53.329	4.992	41.304	1.00 15.46
2440	N	ASP A 432	42.285	-5.672	41.303	1.00 15.55	2485	CA	GLU A 437	54.622	5.123	40.620	1.00 15.46
2441	CA	ASP A 432	42.506	-5.572	42.728	1.00 16.36	2486	C	GLU A 437	55.651	5.927	41.411	1.00 16.03
2442	C	ASP A 432	43.735	-4.744	43.102	1.00 16.54	2487	O	GLU A 437	55.329	7.076	41.747	1.00 17.07
2443	O	ASP A 432	43.956	-4.499	44.305	1.00 15.51	2488	CB	GLU A 437	54.458	5.834	39.263	1.00 15.08
2444	CB	ASP A 432	42.669	-6.988	43.365	1.00 14.88	2489	CG	GLU A 437	55.716	5.978	38.411	1.00 14.65
2445	CG	ASP A 432	41.447	-7.835	43.087	1.00 15.34	2490	CD	GLU A 437	55.493	6.596	37.048	1.00 14.55
2446	OD1	ASP A 432	40.318	-7.267	43.043	1.00 16.21	2491	OE1	GLU A 437	54.648	7.489	36.869	1.00 15.22
2447	OD2	ASP A 432	41.488	-9.064	42.873	1.00 14.61	2492	OE2	GLU A 437	56.087	6.145	36.035	1.00 16.08
2448	N	GLU A 433	44.537	-4.259	42.145	1.00 15.94	2493	N	ALA A 438	56.882	5.394	41.543	1.00 13.55
2449	CA	GLU A 433	45.689	-3.429	42.512	1.00 16.94	2494	CA	ALA A 438	57.878	6.186	42.253	1.00 13.82
2450	C	GLU A 433	45.343	-1.946	42.441	1.00 16.06	2495	O	ALA A 438	59.312	5.910	41.823	1.00 14.91
2451	O	GLU A 433	44.479	-1.513	41.664	1.00 16.07	2496	O	ALA A 438	59.721	4.775	41.558	1.00 13.87
2452	CB	GLU A 433	46.942	-3.630	41.625	1.00 15.85	2497	CB	ALA A 438	57.660	5.898	43.765	1.00 13.69
2453	CG	GLU A 433	47.546	-5.015	41.739	1.00 16.52	2498	N	HIS A 439	60.142	6.969	41.828	1.00 16.29
2454	CD	GLU A 433	48.933	-5.312	41.195	1.00 16.36	2499	CA	HIS A 439	61.572	6.838	41.501	1.00 16.19
2455	OE1	GLU A 433	49.492	-4.536	40.379	1.00 11.53	2500	C	HIS A 439	62.351	6.603	42.805	1.00 16.70
2456	OE2	GLU A 433	49.449	-6.397	41.635	1.00 14.91	2501	O	HIS A 439	62.025	7.212	43.813	1.00 14.31
2457	N	VAL A 434	46.021	-1.168	43.262	1.00 15.28	2502	CB	HIS A 439	62.043	8.086	40.776	1.00 16.30
2458	CA	VAL A 434	46.036	0.299	43.193	1.00 14.14	2503	CG	HIS A 439	63.440	8.147	40.223	1.00 16.75
2459	C	VAL A 434	47.553	0.628	43.106	1.00 15.28	2504	ND1	HIS A 439	64.518	8.470	41.049	1.00 15.99
2460	O	VAL A 434	48.292	0.509	44.136	1.00 13.41	2505	CD2	HIS A 439	63.943	7.963	38.965	1.00 14.58
2461	CB	VAL A 434	45.360	0.930	44.419	1.00 14.74	2506	CE1	HIS A 439	65.624	8.516	40.288	1.00 17.06
2462	CG1	VAL A 434	45.241	2.440	44.130	1.00 14.68	2507	NE2	HIS A 439	65.302	8.221	39.029	1.00 16.41
2463	CG2	VAL A 434	43.954	0.334	44.672	1.00 13.12	2508	N	VAL A 440	63.328	5.687	42.858	1.00 15.20
2464	N	ILE A 435	48.014	1.058	41.947	1.00 14.64	2509	CA	VAL A 440	64.031	5.389	44.106	1.00 15.25
2465	CA	ILE A 435	49.459	1.202	41.665	1.00 13.40	2510	C	VAL A 440	64.653	6.618	44.780	1.00 16.03
2466	C	ILE A 435	49.966	2.607	41.870	1.00 15.38	2511	O	VAL A 440	64.516	6.773	45.999	1.00 16.04
2467	O	ILE A 435	49.312	3.525	41.385	1.00 17.74	2512	CB	VAL A 440	65.116	4.317	43.867	1.00 15.02
2468	CB	ILE A 435	49.775	0.758	40.228	1.00 14.42	2513	CG1	VAL A 440	65.972	4.169	45.128	1.00 16.66
2469	CG1	ILE A 435	49.243	-0.693	40.023	1.00 14.98	2514	CG2	VAL A 440	64.459	2.977	43.508	1.00 15.14
2470	CG2	ILE A 435	51.253	0.888	39.874	1.00 12.09	2515	N	ARG A 441	65.342	7.469	44.034	1.00 16.63

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2516	CA	ARG A 441	65.925	8.698	44.541	1.00	17.10	2561	C	ASP A 446	65.343	15.527	51.856	1.00	18.39
2517	C	ARG A 441	64.899	9.740	45.000	1.00	17.55	2562	O	ASP A 446	65.028	14.618	52.664	1.00	14.79
2518	O	ARG A 441	65.010	10.221	46.170	1.00	17.74	2563	CB	ASP A 446	63.319	15.965	50.406	1.00	17.77
2519	CB	ARG A 441	66.896	9.304	43.501	1.00	14.61	2564	CG	ASP A 446	62.997	17.404	50.598	1.00	19.68
2520	CG	ARG A 441	67.704	10.461	44.088	1.00	16.94	2565	OD1	ASP A 446	62.211	18.007	49.823	1.00	20.47
2521	CD	ARG A 441	68.732	11.060	43.137	1.00	18.60	2566	OD2	ASP A 446	63.527	18.071	51.516	1.00	17.16
2522	NE	ARG A 441	69.386	12.271	43.671	1.00	16.23	2567	N	ALA A 447	65.955	16.640	52.293	1.00	19.59
2523	CZ	ARG A 441	70.470	12.234	44.458	1.00	17.59	2568	CA	ALA A 447	66.372	16.734	53.696	1.00	20.17
2524	NH1	ARG A 441	71.094	11.121	44.855	1.00	17.67	2569	C	ALA A 447	65.444	16.179	55.845	1.00	20.80
2525	NH2	ARG A 441	71.002	13.363	44.893	1.00	17.22	2570	O	ALA A 447	67.086	18.077	53.958	1.00	22.60
2526	N	ASP A 442	63.897	10.087	44.191	1.00	16.68	2571	CB	ALA A 447	63.958	16.873	54.328	1.00	20.17
2527	CA	ASP A 442	62.882	11.067	44.550	1.00	17.07	2572	N	ASN A 448	62.852	16.752	55.303	1.00	19.49
2528	C	ASP A 442	62.150	10.781	45.865	1.00	15.50	2573	CA	ASN A 448	61.062	15.275	55.906	1.00	18.16
2529	O	ASP A 442	61.789	11.686	46.627	1.00	14.92	2574	C	ASN A 448	61.835	17.863	54.959	1.00	18.25
2530	CB	ASP A 442	61.705	11.140	43.534	1.00	16.09	2575	O	ASN A 448	61.103	17.701	53.619	1.00	19.72
2531	CG	ASP A 442	62.092	11.481	42.103	1.00	18.27	2576	CB	ASN A 448	61.019	16.634	52.997	1.00	19.01
2532	OD1	ASP A 442	61.161	11.472	41.265	1.00	16.61	2577	CG	ASN A 448	60.625	18.786	53.028	1.00	18.34
2533	OD2	ASP A 442	63.293	11.722	41.820	1.00	16.36	2578	OD1	ASN A 448	62.630	14.404	54.537	1.00	19.41
2534	N	PHE A 443	61.865	9.519	46.113	1.00	14.50	2579	ND2	ASN A 448	61.917	13.131	54.370	1.00	20.28
2535	CA	PHE A 443	61.090	9.094	47.277	1.00	14.57	2580	N	SER A 449	61.780	12.255	55.599	1.00	20.00
2536	C	PHE A 443	61.629	9.580	48.615	1.00	16.96	2581	CA	SER A 449	60.950	11.332	55.677	1.00	18.80
2537	O	PHE A 443	60.820	9.958	49.474	1.00	15.43	2582	C	SER A 449	62.563	12.336	53.203	1.00	18.80
2538	CB	PHE A 443	61.104	7.553	47.333	1.00	15.23	2583	O	SER A 449	63.731	11.616	53.593	1.00	16.39
2539	CG	PHE A 443	60.077	7.005	48.292	1.00	16.07	2584	CB	SER A 449	62.709	12.410	56.516	1.00	19.28
2540	CD1	PHE A 443	60.475	6.290	49.410	1.00	17.87	2585	N	GLY A 450	62.812	11.662	57.762	1.00	18.69
2541	CD2	PHE A 443	58.722	7.225	48.081	1.00	17.50	2586	C	GLY A 450	63.495	10.312	57.606	1.00	19.34
2542	CE1	PHE A 443	59.546	5.788	50.302	1.00	19.15	2587	CA	GLY A 450	63.580	9.532	58.586	1.00	19.10
2543	CE2	PHE A 443	57.797	6.682	48.961	1.00	19.87	2588	O	GLY A 450	63.897	9.939	56.412	1.00	17.66
2544	CZ	PHE A 443	58.202	5.978	50.077	1.00	19.27	2589	O	MET A 451	64.550	8.650	56.169	1.00	19.49
2545	N	SER A 444	62.941	9.578	48.844	1.00	14.65	2590	N	MET A 451	66.056	8.859	56.152	1.00	21.41
2546	CA	SER A 444	63.491	10.014	50.121	1.00	16.85	2591	CA	MET A 451	66.534	9.886	55.659	1.00	21.59
2547	C	SER A 444	64.692	10.959	50.081	1.00	17.60	2592	C	MET A 451	62.704	7.387	54.938	1.00	18.74
2548	O	SER A 444	65.223	11.288	51.168	1.00	17.78	2593	O	MET A 451	61.951	7.071	53.330	1.00	15.90
2549	CB	SER A 444	64.813	8.072	50.004	1.00	18.93	2594	CB	MET A 451	61.313	8.726	52.990	1.00	16.43
2550	OG	SER A 444	65.083	11.532	48.944	1.00	16.65	2595	CG	MET A 451	66.849	7.964	56.728	1.00	24.96
2551	N	ILE A 445	66.272	12.363	48.864	1.00	17.86	2596	SD	MET A 451	68.292	8.105	56.755	1.00	25.67
2552	CA	ILE A 445	66.133	13.664	49.641	1.00	19.05	2597	CE	MET A 451	69.007	7.729	55.462	1.00	24.98
2553	C	ILE A 445	67.136	14.236	50.089	1.00	19.84	2598	N	LYS A 452	69.976	8.421	55.111	1.00	22.58
2554	O	ILE A 445	66.725	12.704	47.422	1.00	18.82	2599	CA	LYS A 452	68.865	7.134	57.821	1.00	29.87
2555	CB	ILE A 445	68.114	13.345	47.373	1.00	19.76	2600	C	LYS A 452	68.343	7.423	59.227	1.00	38.10
2556	CG1	ILE A 445	65.717	13.625	46.737	1.00	16.03	2601	O	LYS A 452	69.048	6.450	60.162	1.00	38.10
2557	CG2	ILE A 445	69.261	12.451	47.830	1.00	17.68	2602	CB	LYS A 452	68.830	6.729	61.640	1.00	40.92
2558	CD1	ILE A 445	64.944	14.247	49.757	1.00	17.88	2603	CG	LYS A 452					
2559	N	ASP A 446	64.795	15.549	50.429	1.00	19.31	2604	CD	LYS A 452					
2560	CA	ASP A 446						2605	CE	LYS A 452					

2606	NZ	LYS A 452	69.743	5.855	62.443	1.00	43.49	2651	C	LEU A 458	66.370	1.882	52.549	1.00	15.81
2607	N	ASN A 453	68.621	6.628	54.808	1.00	22.30	2652	O	LEU A 458	65.802	1.650	53.569	1.00	14.97
2608	CA	ASN A 453	69.323	6.230	53.583	1.00	22.25	2653	CB	LEU A 458	68.678	0.861	52.699	1.00	17.40
2609	C	ASN A 453	68.792	6.986	52.372	1.00	22.88	2654	CG	LEU A 458	69.584	-0.333	52.378	1.00	17.94
2610	O	ASN A 453	68.213	6.412	51.448	1.00	20.10	2655	CD1	LEU A 458	70.830	-0.312	53.282	1.00	20.17
2611	CB	ASN A 453	69.185	4.732	53.390	1.00	22.17	2656	CD2	LEU A 458	68.866	-1.692	52.511	1.00	17.60
2612	CG	ASN A 453	69.885	3.894	54.438	1.00	22.47	2657	N	ALA A 459	66.132	3.071	51.984	1.00	15.65
2613	OD1	ASN A 453	69.207	3.368	55.345	1.00	26.98	2658	CA	ALA A 459	65.167	4.005	52.608	1.00	16.80
2614	ND2	ASN A 453	71.168	3.715	54.360	1.00	18.00	2659	C	ALA A 459	63.772	3.381	52.772	1.00	18.08
2615	N	LYS A 454	69.120	8.272	52.262	1.00	22.54	2660	O	ALA A 459	63.016	3.656	53.718	1.00	15.52
2616	CA	LYS A 454	68.515	9.200	51.323	1.00	21.14	2661	CB	ALA A 459	65.103	5.260	51.750	1.00	14.58
2617	C	LYS A 454	68.895	8.936	49.881	1.00	20.78	2662	N	PHE A 460	63.361	2.510	51.838	1.00	16.60
2618	O	LYS A 454	70.071	8.790	49.545	1.00	22.89	2663	CA	PHE A 460	62.117	1.786	51.868	1.00	18.35
2619	CB	LYS A 454	68.872	10.638	51.774	1.00	21.38	2664	C	PHE A 460	62.017	0.683	52.942	1.00	19.16
2620	CG	LYS A 454	68.057	11.105	53.013	1.00	23.20	2665	O	PHE A 460	60.944	0.074	53.052	1.00	16.71
2621	CD	LYS A 454	68.334	12.597	53.277	1.00	23.57	2666	CB	PHE A 460	61.813	1.132	50.518	1.00	19.39
2622	CE	LYS A 454	67.796	12.998	54.648	1.00	25.95	2667	CG	PHE A 460	61.495	2.064	49.369	1.00	19.42
2623	NZ	LYS A 454	66.341	12.839	54.758	1.00	26.08	2668	CD1	PHE A 460	60.199	2.051	48.869	1.00	20.23
2624	N	GLY A 455	67.909	8.715	49.012	1.00	19.05	2669	CD2	PHE A 460	59.853	2.859	47.787	1.00	20.33
2625	CA	GLY A 455	68.086	8.463	47.590	1.00	17.30	2670	CE1	PHE A 460	62.162	3.544	47.607	1.00	20.31
2626	C	GLY A 455	68.350	7.013	47.242	1.00	17.20	2671	CE2	PHE A 460	60.847	3.590	47.141	1.00	20.55
2627	O	GLY A 455	68.723	6.665	46.111	1.00	17.53	2672	CZ	PHE A 460	63.086	0.410	53.727	1.00	17.52
2628	N	LYS A 456	68.270	6.123	48.226	1.00	15.28	2673	N	THR A 461	63.041	-0.515	54.824	1.00	17.58
2629	CA	LYS A 456	68.659	4.734	48.032	1.00	16.32	2674	CA	THR A 461	62.842	0.254	56.179	1.00	17.98
2630	C	LYS A 456	67.611	3.650	48.265	1.00	15.37	2675	C	THR A 461	62.824	-0.422	57.195	1.00	17.01
2631	O	LYS A 456	66.603	3.951	48.904	1.00	15.63	2676	O	THR A 461	62.824	-0.422	57.195	1.00	17.01
2632	CB	LYS A 456	69.787	4.424	49.040	1.00	18.28	2677	CB	THR A 461	64.340	-1.338	55.019	1.00	17.81
2633	CG	LYS A 456	70.918	5.434	49.114	1.00	18.06	2678	OG1	THR A 461	65.418	-0.430	55.344	1.00	16.28
2634	CD	LYS A 456	72.081	4.992	48.231	1.00	19.93	2679	OG2	THR A 461	64.706	-2.058	53.713	1.00	18.33
2635	CE	LYS A 456	73.093	6.121	48.121	1.00	20.50	2680	N	GLU A 462	62.820	1.569	56.197	1.00	17.91
2636	NZ	LYS A 456	74.035	5.934	46.985	1.00	18.68	2681	CA	GLU A 462	62.881	2.254	57.509	1.00	18.73
2637	N	TYR A 457	67.870	2.454	47.758	1.00	14.15	2682	C	GLU A 462	61.452	2.526	58.028	1.00	20.80
2638	CA	TYR A 457	66.986	1.341	47.981	1.00	13.53	2683	O	GLU A 462	60.651	3.247	57.389	1.00	17.17
2639	C	TYR A 457	66.678	1.189	49.489	1.00	18.21	2684	CB	GLU A 462	63.597	3.584	57.237	1.00	19.94
2640	O	TYR A 457	65.487	1.011	49.788	1.00	13.29	2685	CG	GLU A 462	65.032	3.372	56.651	1.00	20.13
2641	CB	TYR A 457	67.490	-0.024	47.538	1.00	13.55	2686	CD	GLU A 462	65.759	4.695	56.580	1.00	21.29
2642	CG	TYR A 457	67.956	-0.142	46.075	1.00	14.83	2687	OB1	GLU A 462	65.461	5.602	57.401	1.00	22.06
2643	CD1	TYR A 457	69.241	-0.546	45.761	1.00	15.53	2688	OB2	GLU A 462	66.629	4.885	55.702	1.00	20.07
2644	CD2	TYR A 457	67.107	0.110	45.014	1.00	15.14	2689	N	HIS A 463	61.096	1.977	59.194	1.00	20.54
2645	CE1	TYR A 457	69.663	-0.645	44.409	1.00	15.97	2690	CA	HIS A 463	59.806	2.170	59.831	1.00	22.30
2646	CE2	TYR A 457	67.460	0.018	43.665	1.00	15.67	2691	C	HIS A 463	59.778	3.350	60.778	1.00	22.71
2647	CZ	TYR A 457	68.762	-0.369	43.408	1.00	16.86	2692	O	HIS A 463	60.819	3.655	61.359	1.00	23.44
2648	OH	TYR A 457	69.165	-0.482	42.066	1.00	18.18	2693	CB	HIS A 463	59.476	0.918	60.666	1.00	24.53
2649	N	LEU A 458	67.603	1.255	50.450	1.00	17.70	2694	CG	HIS A 463	59.062	-0.209	59.775	1.00	26.84
2650	CA	LEU A 458	67.335	0.919	51.869	1.00	18.01	2695	ND1	HIS A 463	59.954	-1.062	59.187	1.00	29.88

2696	CD2	HIS	A	463	57.841	-0.611	59.362	1.00	28.11	2741	O	HIS	A	470	53.713	13.036	61.986	1.00	25.40
2697	CE1	HIS	A	463	59.315	-1.954	58.450	1.00	29.51	2742	CB	HIS	A	470	54.351	14.933	63.968	1.00	35.53
2698	NE2	HIS	A	463	58.029	-1.696	58.538	1.00	30.87	2743	CG	HIS	A	470	54.966	13.762	64.690	1.00	41.88
2699	N	GLY	A	464	58.637	3.962	61.066	1.00	23.85	2744	ND1	HIS	A	470	54.293	12.781	65.341	1.00	44.60
2700	CA	GLY	A	464	58.547	5.049	62.031	1.00	22.89	2745	CD2	HIS	A	470	56.338	13.553	64.868	1.00	44.13
2701	C	GLY	A	464	59.042	6.398	61.558	1.00	23.91	2746	CE1	HIS	A	470	55.239	11.999	65.896	1.00	45.27
2702	O	GLY	A	464	59.256	7.293	62.406	1.00	21.28	2747	NE2	HIS	A	470	56.472	12.438	65.630	1.00	45.71
2703	N	THR	A	465	59.227	6.617	60.250	1.00	21.74	2748	N	VAL	A	471	54.101	14.443	60.279	1.00	24.01
2704	CA	THR	A	465	59.815	7.888	59.806	1.00	21.41	2749	CA	VAL	A	471	53.376	13.539	59.370	1.00	22.37
2705	C	THR	A	465	58.782	8.990	59.735	1.00	21.03	2750	C	VAL	A	471	54.211	12.254	59.214	1.00	21.98
2706	O	THR	A	465	57.602	8.744	59.460	1.00	23.25	2751	O	VAL	A	471	55.442	12.318	59.299	1.00	20.13
2707	CB	THR	A	465	60.563	7.738	58.467	1.00	22.09	2752	CB	VAL	A	471	53.104	14.132	57.982	1.00	21.65
2708	CG1	THR	A	465	59.630	7.327	57.447	1.00	20.70	2753	CG1	VAL	A	471	52.190	15.365	58.015	1.00	19.93
2709	CG2	THR	A	465	61.643	6.667	58.699	1.00	21.72	2754	CG2	VAL	A	471	54.419	14.466	57.278	1.00	20.15
2710	N	LYS	A	466	59.185	10.189	60.070	1.00	19.33	2755	N	LYS	A	472	53.542	11.139	58.935	1.00	19.69
2711	CA	LYS	A	466	58.343	11.334	60.285	1.00	21.71	2756	CA	LYS	A	472	54.244	9.876	58.649	1.00	18.37
2712	C	LYS	A	466	58.905	12.549	59.557	1.00	21.36	2757	C	LYS	A	472	54.846	9.942	57.237	1.00	17.74
2713	O	LYS	A	466	60.121	12.630	59.456	1.00	22.34	2758	O	LYS	A	472	54.211	10.506	56.321	1.00	17.56
2714	CB	LYS	A	466	58.316	11.761	61.775	1.00	22.16	2759	CB	LYS	A	472	53.212	8.750	58.700	1.00	21.16
2715	CG	LYS	A	466	57.913	10.655	62.722	1.00	25.69	2760	CG	LYS	A	472	52.495	8.535	60.043	1.00	20.15
2716	CD	LYS	A	466	56.511	10.112	62.448	1.00	27.19	2761	CD	LYS	A	472	51.529	7.341	59.924	1.00	21.24
2717	CE	LYS	A	466	56.168	9.053	63.502	1.00	29.76	2762	CE	LYS	A	472	51.192	6.810	61.317	1.00	25.17
2718	NZ	LYS	A	466	54.932	8.298	63.127	1.00	29.77	2763	NZ	LYS	A	472	57.096	5.690	61.273	1.00	26.92
2719	N	GLY	A	467	58.029	13.410	59.087	1.00	20.73	2764	N	THR	A	473	56.073	9.506	56.991	1.00	16.26
2720	CA	GLY	A	467	58.437	14.611	58.385	1.00	22.16	2765	CA	THR	A	473	56.650	9.508	55.639	1.00	17.04
2721	C	GLY	A	467	57.855	15.833	59.110	1.00	23.57	2766	C	THR	A	473	57.096	8.108	55.226	1.00	16.39
2722	O	GLY	A	467	57.559	15.770	60.300	1.00	21.29	2767	O	THR	A	473	56.881	7.201	56.041	1.00	14.08
2723	N	PRO	A	468	57.742	16.944	58.387	1.00	24.04	2768	CB	THR	A	473	57.916	10.402	55.585	1.00	17.28
2724	CA	PRO	A	468	57.264	18.188	58.952	1.00	24.86	2769	CG1	THR	A	473	58.862	9.885	56.543	1.00	17.62
2725	C	PRO	A	468	55.921	18.023	59.638	1.00	26.71	2770	CG2	THR	A	473	57.590	11.827	56.000	1.00	15.36
2726	O	PRO	A	468	55.032	17.290	59.223	1.00	24.09	2771	N	GLY	A	474	57.706	7.921	54.044	1.00	15.08
2727	CB	PRO	A	468	57.252	19.135	57.761	1.00	24.51	2772	CA	GLY	A	474	58.229	6.588	53.720	1.00	15.08
2728	CG	PRO	A	468	58.442	18.647	56.967	1.00	24.08	2773	C	GLY	A	474	57.174	5.503	53.681	1.00	17.27
2729	CD	PRO	A	468	58.260	17.127	57.004	1.00	23.34	2774	O	GLY	A	474	55.985	5.776	53.434	1.00	15.09
2730	N	ASP	A	469	55.809	18.622	60.845	1.00	28.85	2775	N	ILE	A	474	57.568	4.262	53.897	1.00	18.67
2731	CA	ASP	A	469	54.568	18.580	61.605	1.00	31.00	2776	CA	ILE	A	475	56.630	3.138	53.914	1.00	20.49
2732	C	ASP	A	469	54.190	17.167	62.012	1.00	29.54	2777	C	ILE	A	475	55.474	3.256	54.907	1.00	19.29
2733	O	ASP	A	469	53.005	16.831	62.142	1.00	25.09	2778	O	ILE	A	475	54.377	2.749	54.563	1.00	18.42
2734	CB	ASP	A	469	53.429	19.166	60.762	1.00	35.81	2779	CB	ILE	A	475	57.414	1.826	54.113	1.00	22.81
2735	CG	ASP	A	469	53.461	20.687	60.704	1.00	41.18	2780	CG1	ILE	A	475	56.478	0.702	53.724	1.00	24.37
2736	OD1	ASP	A	469	54.229	21.361	61.442	1.00	42.60	2781	CG2	ILE	A	475	57.885	1.646	55.592	1.00	21.69
2737	OD2	ASP	A	469	52.675	21.251	59.899	1.00	42.71	2782	CD1	ILE	A	475	57.108	-0.882	53.618	1.00	28.52
2738	N	HIS	A	470	55.216	16.314	62.194	1.00	27.09	2783	N	ASP	A	476	55.616	3.969	56.026	1.00	17.17
2739	CA	HIS	A	470	54.991	14.943	62.567	1.00	29.90	2784	CA	ASP	A	476	54.413	4.168	56.891	1.00	17.44
2740	C	HIS	A	470	54.158	14.124	61.571	1.00	27.51	2785	C	ASP	A	476	53.387	5.060	56.185	1.00	16.48

2766	O	ASP	A	476	52.197	4.895	56.429	1.00	15.25	2831	N	GLY	A	482	46.845	3.526	51.664	1.00	15.48
2767	CB	ASP	A	476	54.756	4.796	58.234	1.00	16.38	2832	CA	GLY	A	482	46.042	2.419	51.161	1.00	15.68
2768	CG	ASP	A	476	55.480	3.874	59.211	1.00	18.13	2833	C	GLY	A	482	46.507	1.767	49.851	1.00	16.09
2769	OD1	ASP	A	476	55.930	4.354	60.259	1.00	17.91	2834	O	GLY	A	482	45.908	0.771	49.461	1.00	14.56
2770	OD2	ASP	A	476	55.639	2.680	58.915	1.00	16.55	2835	N	ILE	A	483	47.483	2.333	49.124	1.00	15.13
2771	N	SER	A	477	53.766	6.034	55.354	1.00	16.25	2836	CA	ILE	A	483	47.942	1.737	47.849	1.00	15.05
2772	CA	SER	A	477	52.848	6.880	54.629	1.00	16.55	2837	C	ILE	A	483	48.385	0.301	48.077	1.00	15.90
2773	C	SER	A	477	52.108	6.065	53.549	1.00	18.34	2838	O	ILE	A	483	48.723	-0.099	49.196	1.00	17.41
2774	O	SER	A	477	50.912	6.237	53.283	1.00	19.12	2839	CB	ILE	A	483	49.000	2.569	47.120	1.00	14.77
2775	CB	SER	A	477	53.532	8.086	53.987	1.00	15.71	2840	CG1	ILE	A	483	50.358	2.717	47.833	1.00	15.86
2776	OG	SER	A	477	52.610	8.857	53.192	1.00	17.49	2841	CG2	ILE	A	483	48.429	3.967	46.809	1.00	15.27
2777	N	LEU	A	478	52.825	5.184	52.841	1.00	18.20	2842	CD1	ILE	A	483	51.356	1.531	47.671	1.00	13.17
2778	CA	LEU	A	478	52.237	4.299	51.853	1.00	17.44	2843	N	THR	A	484	48.308	-0.555	47.050	1.00	15.28
2779	C	LEU	A	478	51.154	3.403	52.475	1.00	19.05	2844	CA	THR	A	484	48.633	-1.952	47.213	1.00	15.28
2800	O	LEU	A	478	50.062	3.242	51.912	1.00	16.99	2845	C	THR	A	484	49.933	-2.359	46.538	1.00	15.86
2801	CB	LEU	A	478	53.296	3.419	51.195	1.00	17.36	2846	O	THR	A	484	50.410	-3.469	46.796	1.00	13.72
2802	CG	LEU	A	478	54.412	4.051	50.367	1.00	18.83	2847	CB	THR	A	484	47.549	-2.863	46.532	1.00	16.48
2803	CD1	LEU	A	478	55.262	2.927	49.763	1.00	20.70	2848	OG1	THR	A	484	47.638	-2.693	45.102	1.00	16.43
2804	CD2	LEU	A	478	53.898	5.003	49.304	1.00	17.67	2849	CG2	THR	A	484	46.150	-2.505	47.003	1.00	16.06
2805	N	LYS	A	479	51.418	2.843	53.647	1.00	20.29	2850	N	THR	A	485	50.443	-1.551	45.605	1.00	14.91
2806	CA	LYS	A	479	50.448	2.085	54.413	1.00	23.91	2851	CA	THR	A	485	51.595	-1.965	44.783	1.00	15.42
2807	C	LYS	A	479	49.209	2.910	54.724	1.00	22.75	2852	C	THR	A	485	52.427	-0.757	44.384	1.00	15.53
2808	O	LYS	A	479	48.056	2.535	54.473	1.00	23.72	2853	O	THR	A	485	51.863	0.244	43.919	1.00	15.10
2809	CB	LYS	A	479	51.049	1.642	55.759	1.00	27.33	2854	CB	THR	A	485	51.065	-2.655	43.513	1.00	15.83
2810	CG	LYS	A	479	50.226	0.539	56.358	1.00	32.76	2855	OG1	THR	A	485	50.004	-3.584	43.802	1.00	16.38
2811	CD	LYS	A	479	50.636	-0.179	57.602	1.00	37.03	2856	CG2	THR	A	485	52.059	-3.489	42.695	1.00	16.14
2812	CE	LYS	A	479	52.051	-0.291	58.088	1.00	40.23	2857	N	VAL	A	486	53.764	-0.790	44.555	1.00	14.94
2813	NZ	LYS	A	479	52.935	-1.004	57.114	1.00	42.37	2858	CA	VAL	A	486	54.652	0.297	44.134	1.00	12.74
2814	N	GLU	A	480	49.388	4.126	55.242	1.00	21.40	2859	C	VAL	A	486	55.245	0.001	42.748	1.00	14.15
2815	CA	GLU	A	480	48.229	4.920	55.588	1.00	22.52	2860	O	VAL	A	486	55.788	-1.134	42.601	1.00	14.85
2816	C	GLU	A	480	47.449	5.378	54.364	1.00	19.27	2861	CB	VAL	A	486	55.857	0.483	45.082	1.00	14.01
2817	O	GLU	A	480	46.229	5.531	54.458	1.00	16.95	2862	CG1	VAL	A	486	56.783	1.610	44.531	1.00	12.76
2818	CB	GLU	A	480	48.490	6.066	56.547	1.00	25.40	2863	CG2	VAL	A	486	55.303	0.961	46.438	1.00	15.43
2819	CG	GLU	A	480	49.133	7.273	55.983	1.00	28.08	2864	N	GLN	A	487	55.159	0.899	41.798	1.00	12.39
2820	CD	GLU	A	480	49.042	8.444	56.945	1.00	30.33	2865	CA	GLN	A	487	55.823	0.699	40.507	1.00	13.69
2821	OE1	GLU	A	480	48.009	8.573	57.618	1.00	33.89	2866	C	GLN	A	487	57.124	1.507	40.520	1.00	14.02
2822	OE2	GLU	A	480	49.967	9.261	57.025	1.00	26.83	2867	O	GLN	A	487	57.008	2.717	40.530	1.00	15.37
2823	N	LEU	A	481	48.091	5.482	53.220	1.00	19.95	2868	CB	GLN	A	487	54.975	1.132	39.304	1.00	14.53
2824	CA	LEU	A	481	47.406	5.891	51.984	1.00	16.96	2869	CG	GLN	A	487	55.555	0.810	37.899	1.00	14.85
2825	C	LEU	A	481	46.484	4.792	51.463	1.00	17.11	2870	CD	GLN	A	487	54.658	1.489	36.844	1.00	15.25
2826	O	LEU	A	481	45.404	5.121	50.925	1.00	15.46	2871	OE1	GLN	A	487	53.542	0.999	36.600	1.00	12.63
2827	CR	LEU	A	481	48.502	6.240	50.976	1.00	17.20	2872	NE2	GLN	A	487	55.086	2.600	36.263	1.00	14.69
2828	CG	LEU	A	481	48.070	6.823	49.640	1.00	17.62	2873	N	LEU	A	488	58.291	0.856	40.520	1.00	13.77
2829	CD1	LEU	A	481	47.221	8.098	49.831	1.00	16.14	2874	CA	LEU	A	488	59.537	1.560	40.518	1.00	15.79
2830	CD2	LEU	A	481	49.273	7.277	48.811	1.00	14.35	2875	C	LEU	A	488	60.035	1.987	39.152	1.00	15.05

2876	O	LEU A 488	60.073	1.122	38.294	1.00	15.87	2921	OE2	GLU A 493	74.095	-0.479	37.541	1.00	19.62
2877	CB	LEU A 488	60.595	0.684	41.146	1.00	14.51	2922	N	PHE A 494	71.755	1.230	34.238	1.00	15.08
2878	CG	LEU A 488	60.575	0.236	42.618	1.00	16.06	2923	CA	PHE A 494	71.716	2.064	33.051	1.00	17.22
2879	CD1	LEU A 488	61.575	-0.885	42.971	1.00	15.85	2924	C	PHE A 494	73.040	2.834	32.904	1.00	17.93
2880	CD2	LEU A 488	60.742	1.336	43.642	1.00	11.74	2925	O	PHE A 494	73.846	2.871	33.840	1.00	17.61
2881	N	GLN A 489	60.487	3.246	39.045	1.00	15.31	2926	CB	PHE A 494	70.494	2.985	33.079	1.00	15.05
2882	CA	GLN A 489	61.188	3.679	37.812	1.00	14.87	2927	CG	PHE A 494	70.209	3.732	34.347	1.00	13.69
2883	C	GLN A 489	62.425	2.807	37.665	1.00	14.33	2928	CD1	PHE A 494	69.309	3.238	35.283	1.00	13.97
2884	O	GLN A 489	62.859	2.155	38.606	1.00	14.60	2929	CD2	PHE A 494	70.814	4.964	34.603	1.00	14.09
2885	CB	GLN A 489	61.403	5.188	37.805	1.00	15.88	2930	CE1	PHE A 494	69.008	3.927	36.442	1.00	13.34
2886	CG	GLN A 489	60.080	5.982	37.617	1.00	16.42	2931	CE2	PHE A 494	70.548	5.662	35.766	1.00	13.82
2887	CD	GLN A 489	60.312	7.400	37.152	1.00	16.75	2932	CZ	PHE A 494	69.650	5.128	36.706	1.00	14.68
2888	OE1	GLN A 489	60.684	7.691	35.982	1.00	19.64	2933	N	ASN A 495	73.262	3.489	31.758	1.00	17.56
2889	NE2	GLN A 489	60.177	8.368	38.027	1.00	14.55	2934	CA	ASN A 495	74.549	4.074	31.443	1.00	19.21
2890	N	PRO A 490	63.045	2.689	36.494	1.00	14.20	2935	C	ASN A 495	74.759	5.505	31.926	1.00	18.67
2891	CA	PRO A 490	64.089	1.703	36.225	1.00	13.53	2936	O	ASN A 495	75.915	5.887	32.059	1.00	17.87
2892	C	PRO A 490	65.155	1.438	37.241	1.00	14.81	2937	CB	ASN A 495	74.850	4.084	29.931	1.00	17.20
2893	O	PRO A 490	65.895	2.388	37.605	1.00	15.34	2938	CG	ASN A 495	76.266	4.473	29.570	1.00	20.20
2894	CB	PRO A 490	64.707	2.269	34.906	1.00	13.82	2939	OD1	ASN A 495	77.257	3.802	29.891	1.00	18.77
2895	CG	PRO A 490	63.479	2.776	34.197	1.00	15.17	2940	ND2	ASN A 495	76.482	5.618	28.938	1.00	19.57
2896	CD	PRO A 490	62.691	3.502	35.299	1.00	11.82	2941	N	SER A 496	73.715	6.299	32.041	1.00	17.59
2897	N	VAL A 491	65.780	0.210	37.709	1.00	14.57	2942	CA	SER A 496	73.827	7.723	32.297	1.00	17.54
2898	CA	VAL A 491	66.362	-0.156	38.655	1.00	16.33	2943	C	SER A 496	74.342	6.127	33.652	1.00	18.68
2899	C	VAL A 491	67.293	-1.160	37.970	1.00	17.32	2944	O	SER A 496	74.638	9.331	33.798	1.00	18.94
2900	O	VAL A 491	68.202	-1.714	38.584	1.00	17.98	2945	CB	SER A 496	72.487	8.433	32.001	1.00	19.07
2901	CB	VAL A 491	65.792	-0.718	39.976	1.00	15.46	2946	OG	SER A 496	71.377	7.889	32.711	1.00	17.68
2902	CG1	VAL A 491	64.974	0.369	40.708	1.00	13.55	2947	N	ILE A 497	74.441	7.273	34.670	1.00	16.74
2903	CG2	VAL A 491	64.915	-1.944	39.688	1.00	14.62	2948	CA	ILE A 497	75.071	7.777	35.908	1.00	17.05
2904	N	GLU A 492	67.092	-1.504	36.697	1.00	18.44	2949	C	ILE A 497	76.434	7.104	36.029	1.00	17.86
2905	CA	GLU A 492	68.031	-2.245	35.863	1.00	16.40	2950	O	ILE A 497	76.528	5.880	35.928	1.00	16.60
2906	C	GLU A 492	69.156	-1.271	35.451	1.00	17.63	2951	CB	ILE A 497	74.203	7.473	37.156	1.00	18.85
2907	O	GLU A 492	68.937	-0.141	34.964	1.00	15.32	2952	CG1	ILE A 497	72.950	8.366	37.145	1.00	18.39
2908	CB	GLU A 492	67.459	-2.927	34.598	1.00	15.59	2953	CG2	ILE A 497	75.033	7.586	38.435	1.00	16.11
2909	CG	GLU A 492	66.412	-4.003	34.981	1.00	16.27	2954	CD1	ILE A 497	71.845	8.001	38.145	1.00	18.90
2910	CD	GLU A 492	65.731	-4.713	33.824	1.00	16.24	2955	N	ASP A 498	77.478	7.888	36.227	1.00	18.34
2911	OE1	GLU A 492	65.079	-5.765	33.984	1.00	15.93	2956	CA	ASP A 498	78.806	7.346	36.522	1.00	19.14
2912	OE2	GLU A 492	65.871	-4.235	32.678	1.00	16.98	2957	C	ASP A 498	78.770	6.898	37.971	1.00	17.01
2913	N	GLU A 493	70.400	-1.716	35.653	1.00	17.89	2958	O	ASP A 498	78.609	7.762	38.858	1.00	15.12
2914	CA	GLU A 493	71.592	-0.901	35.413	1.00	18.19	2959	CB	ASP A 498	79.851	8.458	36.364	1.00	21.90
2915	C	GLU A 493	71.592	-0.092	34.107	1.00	17.67	2960	CG	ASP A 498	81.295	8.069	36.759	1.00	24.10
2916	O	GLU A 493	71.579	-0.640	33.012	1.00	15.24	2961	OD1	ASP A 498	82.155	8.832	36.229	1.00	23.49
2917	CB	GLU A 493	72.869	-1.773	35.447	1.00	18.34	2962	OD2	ASP A 498	81.615	7.096	37.480	1.00	19.87
2918	CG	GLU A 493	74.173	-1.020	35.230	1.00	18.92	2963	N	GLU A 499	79.011	5.646	38.280	1.00	16.55
2919	CD	GLU A 493	74.742	-0.344	36.455	1.00	19.23	2964	CA	GLU A 499	78.977	5.108	39.632	1.00	19.92
2920	OE1	GLU A 493	75.796	0.334	36.325	1.00	17.41	2965	C	GLU A 499	79.988	5.691	40.614	1.00	21.17

2966	O	GLU A 499	79.775	5.543	41.836	1.00	20.23	3011	CA	TYR A 505	70.198	12.564	38.498	1.00	20.51
2967	CB	GLU A 499	79.090	3.565	39.610	1.00	18.52	3012	C	TYR A 505	69.839	11.991	37.135	1.00	20.40
2968	CG	GLU A 499	77.783	3.044	38.948	1.00	17.11	3013	O	TYR A 505	70.037	12.679	36.103	1.00	19.81
2969	CD	GLU A 499	77.715	1.561	38.901	1.00	19.30	3014	CB	TYR A 505	69.281	13.777	38.795	1.00	19.30
2970	OE1	GLU A 499	78.782	0.866	38.946	1.00	18.97	3015	CG	TYR A 505	67.814	13.347	38.862	1.00	19.19
2971	OE2	GLU A 499	76.609	0.973	38.775	1.00	18.01	3016	CD1	TYR A 505	67.241	13.027	40.115	1.00	17.54
2972	N	THR A 500	81.008	6.404	40.126	1.00	20.80	3017	CD2	TYR A 505	67.023	13.226	37.730	1.00	16.46
2973	CA	THR A 500	81.940	7.053	41.057	1.00	23.34	3018	CE1	TYR A 505	65.931	12.559	40.199	1.00	16.03
2974	C	THR A 500	81.372	8.400	41.497	1.00	24.20	3019	CE2	TYR A 505	65.697	12.777	37.831	1.00	16.62
2975	O	THR A 500	82.015	9.077	42.287	1.00	24.37	3020	CZ	TYR A 505	65.163	12.442	39.058	1.00	17.37
2976	CB	THR A 500	83.342	7.317	40.473	1.00	21.92	3021	OH	TYR A 505	63.859	11.975	39.132	1.00	16.33
2977	OG1	THR A 500	83.230	8.244	39.379	1.00	20.76	3022	N	ASN A 506	69.117	10.864	37.112	1.00	19.02
2978	CG2	THR A 500	84.023	6.044	39.986	1.00	22.58	3023	CA	ASN A 506	68.525	10.394	35.854	1.00	17.54
2979	N	GLN A 501	80.313	8.895	40.895	1.00	26.63	3024	C	ASN A 506	67.354	9.433	36.132	1.00	16.94
2980	CA	GLN A 501	79.580	10.111	41.217	1.00	29.35	3025	O	ASN A 506	67.448	8.585	37.023	1.00	15.04
2981	C	GLN A 501	78.081	9.780	41.293	1.00	29.18	3026	CB	ASN A 506	69.538	9.697	34.935	1.00	17.11
2982	O	GLN A 501	77.286	10.114	40.421	1.00	28.10	3027	CG	ASN A 506	69.102	9.692	33.481	1.00	19.56
2983	CB	GLN A 501	79.695	11.145	40.089	1.00	32.33	3028	OD1	ASN A 506	68.283	8.880	33.019	1.00	18.08
2984	CG	GLN A 501	81.113	11.471	39.637	1.00	36.70	3029	ND2	ASN A 506	69.679	10.641	32.729	1.00	18.09
2985	CD	GLN A 501	81.850	12.239	40.710	1.00	41.32	3030	N	TRP A 507	66.363	9.479	35.216	1.00	14.78
2986	OE1	GLN A 501	81.235	12.619	41.723	1.00	43.52	3031	CA	TRP A 507	65.263	8.515	35.282	1.00	14.79
2987	NE2	GLN A 501	83.153	12.497	40.515	1.00	44.21	3032	C	TRP A 507	65.716	7.096	34.995	1.00	14.58
2988	N	PRO A 502	77.652	9.030	42.297	1.00	29.53	3033	O	TRP A 507	65.101	6.151	35.466	1.00	12.62
2989	CA	PRO A 502	76.292	8.507	42.359	1.00	28.54	3034	CB	TRP A 507	64.189	8.879	34.236	1.00	13.89
2990	C	PRO A 502	75.175	9.471	42.670	1.00	28.87	3035	CG	TRP A 507	63.208	9.944	34.647	1.00	13.96
2991	O	PRO A 502	74.004	9.050	42.701	1.00	30.15	3036	CD1	TRP A 507	63.021	10.504	35.878	1.00	13.86
2992	CB	PRO A 502	76.406	7.392	43.399	1.00	26.18	3037	CD2	TRP A 507	62.268	10.598	33.765	1.00	13.76
2993	CG	PRO A 502	77.510	7.853	44.309	1.00	27.23	3038	NE1	TRP A 507	62.035	11.509	35.797	1.00	14.63
2994	CD	PRO A 502	78.477	8.622	43.471	1.00	27.08	3039	CE2	TRP A 507	61.572	11.557	34.520	1.00	14.09
2995	N	ASP A 503	75.432	10.751	42.881	1.00	28.94	3040	CE3	TRP A 507	62.006	10.488	32.396	1.00	14.36
2996	CA	ASP A 503	74.380	11.709	43.179	1.00	29.84	3041	CE2	TRP A 507	60.623	12.410	33.943	1.00	15.35
2997	C	ASP A 503	73.930	12.521	41.976	1.00	28.92	3042	CZ3	TRP A 507	61.039	11.314	31.837	1.00	16.79
2998	O	ASP A 503	73.125	13.446	42.132	1.00	30.62	3043	CH2	TRP A 507	60.359	12.283	32.620	1.00	14.29
2999	CB	ASP A 503	74.783	12.642	44.344	1.00	29.97	3044	N	GLY A 508	66.779	6.933	34.176	1.00	14.06
3000	CG	ASP A 503	74.845	11.877	45.654	1.00	31.52	3045	CA	GLY A 508	67.280	5.621	33.845	1.00	14.97
3001	OD1	ASP A 503	74.016	10.975	45.912	1.00	29.14	3046	C	GLY A 508	66.688	4.906	32.664	1.00	13.65
3002	OD2	ASP A 503	75.783	12.160	46.439	1.00	33.43	3047	O	GLY A 508	66.794	3.661	32.610	1.00	13.65
3003	N	THR A 504	74.384	12.204	40.790	1.00	28.14	3048	N	TYR A 509	66.161	5.623	31.664	1.00	15.66
3004	CA	THR A 504	73.894	12.795	39.547	1.00	28.02	3049	CA	TYR A 509	65.673	5.037	30.419	1.00	16.40
3005	C	THR A 504	72.464	12.303	39.332	1.00	25.44	3050	C	TYR A 509	66.771	4.746	29.389	1.00	16.91
3006	O	THR A 504	72.090	11.307	39.988	1.00	26.41	3051	O	TYR A 509	66.436	4.451	28.241	1.00	16.03
3007	CB	THR A 504	74.817	12.287	38.421	1.00	30.26	3052	CB	TYR A 509	64.471	5.812	29.758	1.00	14.79
3008	OG1	THR A 504	74.365	12.697	37.137	1.00	34.86	3053	CG	TYR A 509	63.288	5.731	30.729	1.00	17.63
3009	CG2	THR A 504	74.853	10.784	38.452	1.00	32.35	3054	CD1	TYR A 509	62.469	4.608	30.816	1.00	15.29
3010	N	TYR A 505	71.617	12.976	38.574	1.00	22.48	3055	CD2	TYR A 509	63.037	6.779	31.616	1.00	17.85

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3056	CE1 TYR A 509	61.434	4.549	31.726	1.00 14.88	3101	CD2 TYR A 514	69.604	-5.279	28.597	1.00 19.59
3057	CE2 TYR A 509	62.012	6.715	32.540	1.00 17.47	3102	CE1 TYR A 514	67.289	-3.734	28.595	1.00 18.29
3058	CZ TYR A 509	61.210	5.585	32.587	1.00 18.26	3103	CE2 TYR A 514	69.328	-4.444	27.514	1.00 19.38
3059	OH TYR A 509	60.204	5.532	33.541	1.00 18.82	3104	CZ TYR A 514	68.167	-3.696	27.521	1.00 19.34
3060	N ASP A 510	68.021	4.495	29.735	1.00 16.31	3105	OH TYR A 514	67.857	-2.887	26.450	1.00 22.29
3061	CA ASP A 510	69.142	4.129	28.870	1.00 18.35	3106	N ASN A 515	70.493	-7.389	33.643	1.00 17.63
3062	C ASP A 510	69.891	2.912	29.392	1.00 17.34	3107	CA ASN A 515	70.280	-8.339	34.745	1.00 17.34
3063	O ASP A 510	71.041	2.945	29.873	1.00 20.99	3108	C ASN A 515	70.978	-7.906	36.018	1.00 17.54
3064	CB ASP A 510	70.120	5.322	28.723	1.00 19.25	3109	O ASN A 515	71.187	-8.752	36.913	1.00 18.12
3065	CG ASP A 510	70.746	5.804	30.000	1.00 21.01	3110	CB ASN A 515	70.786	-9.703	34.185	1.00 16.85
3066	OD1 ASP A 510	70.057	5.942	31.032	1.00 21.87	3111	CG ASN A 515	69.974	-10.095	32.944	1.00 18.64
3067	OD2 ASP A 510	71.991	6.068	30.056	1.00 23.52	3112	OD1 ASN A 515	70.465	-10.350	31.826	1.00 21.03
3068	N PRO A 511	69.294	1.752	29.370	1.00 16.56	3113	ND2 ASN A 515	68.680	-10.119	33.147	1.00 11.82
3069	CA PRO A 511	69.789	0.507	29.915	1.00 17.26	3114	N VAL A 516	71.402	-6.561	36.141	1.00 14.31
3070	O PRO A 511	71.112	0.019	29.272	1.00 17.06	3115	CA VAL A 516	72.083	-6.138	37.344	1.00 15.74
3071	C PRO A 511	71.327	0.259	28.077	1.00 16.16	3116	C VAL A 516	71.301	-4.960	37.911	1.00 16.74
3072	CB PRO A 511	68.730	-0.564	29.675	1.00 16.53	3117	O VAL A 516	70.892	-4.053	37.176	1.00 16.35
3073	CG PRO A 511	67.898	-0.001	28.531	1.00 17.61	3118	CB VAL A 516	73.478	-5.606	36.838	1.00 16.38
3074	CD PRO A 511	67.914	1.498	28.752	1.00 17.12	3119	CG1 VAL A 516	74.289	-4.915	37.924	1.00 15.90
3075	N ARG A 512	71.925	-0.624	30.102	1.00 16.69	3120	CG2 VAL A 516	74.293	-6.720	36.163	1.00 15.48
3076	CA ARG A 512	73.212	-1.174	29.634	1.00 16.56	3121	N PRO A 517	71.121	-4.832	39.223	1.00 17.59
3077	C ARG A 512	73.392	-2.618	30.065	1.00 16.11	3122	CA PRO A 517	70.522	-3.863	39.846	1.00 15.46
3078	O ARG A 512	73.824	-3.472	29.278	1.00 16.43	3123	C PRO A 517	71.370	-2.408	39.664	1.00 16.15
3079	CB ARG A 512	74.394	-0.275	30.088	1.00 18.15	3124	O PRO A 517	72.601	-2.451	39.870	1.00 17.59
3080	CG ARG A 512	75.778	-0.703	29.616	1.00 18.63	3125	CB PRO A 517	70.481	-4.030	41.330	1.00 16.03
3081	CD ARG A 512	76.929	0.127	30.219	1.00 19.47	3126	CG PRO A 517	70.630	-5.532	41.363	1.00 16.94
3082	NE ARG A 512	77.011	-0.045	31.687	1.00 20.90	3127	CD PRO A 517	71.656	-5.777	40.261	1.00 15.72
3083	CZ ARG A 512	77.354	0.937	32.563	1.00 20.85	3128	N GLU A 518	70.756	-1.245	39.475	1.00 13.80
3084	NH1 ARG A 512	77.328	0.708	33.877	1.00 20.82	3129	CA GLU A 518	71.457	0.025	39.340	1.00 15.14
3085	NH2 ARG A 512	77.653	2.184	32.233	1.00 19.17	3130	C GLU A 518	72.366	0.288	40.567	1.00 15.73
3086	N ASN A 513	73.175	-2.970	31.326	1.00 15.21	3131	O GLU A 518	71.844	0.352	41.694	1.00 14.71
3087	CA ASN A 513	73.323	-4.307	31.896	1.00 14.14	3132	CB GLU A 518	70.444	1.149	39.065	1.00 14.95
3088	C ASN A 513	71.957	-4.696	32.471	1.00 15.83	3133	CG GLU A 518	71.065	2.558	39.118	1.00 15.19
3089	O ASN A 513	71.562	-4.414	33.623	1.00 14.75	3134	CD GLU A 518	72.139	2.790	38.080	1.00 17.66
3090	CB ASN A 513	74.425	-4.304	32.991	1.00 13.68	3135	OE1 GLU A 518	72.129	2.189	36.974	1.00 16.65
3091	CG ASN A 513	75.722	-3.670	32.503	1.00 15.65	3136	OE2 GLU A 518	73.093	3.591	38.350	1.00 17.95
3092	OD1 ASN A 513	75.960	-2.463	32.702	1.00 13.93	3137	N GLY A 519	73.671	0.589	40.305	1.00 15.19
3093	ND2 ASN A 513	76.592	-4.443	31.817	1.00 13.93	3138	CA GLY A 519	74.567	0.786	41.499	1.00 15.74
3094	N TYR A 514	71.137	-5.398	31.687	1.00 16.49	3139	C GLY A 519	74.412	2.112	42.221	1.00 15.83
3095	CA TYR A 514	69.742	-5.666	32.068	1.00 17.77	3140	O GLY A 519	74.575	2.196	43.455	1.00 14.13
3096	C TYR A 514	69.496	-6.572	33.280	1.00 18.89	3141	N ALA A 520	73.905	3.163	41.577	1.00 16.04
3097	O TYR A 514	68.398	-6.564	33.865	1.00 16.26	3142	CA ALA A 520	73.780	4.471	42.239	1.00 18.29
3098	CB TYR A 514	69.017	-6.266	30.861	1.00 18.16	3143	C ALA A 520	72.771	4.499	43.381	1.00 18.95
3099	CG TYR A 514	68.726	-5.341	29.689	1.00 18.97	3144	O ALA A 520	72.856	5.422	44.196	1.00 16.80
3100	CD1 TYR A 514	67.565	-4.560	29.672	1.00 18.42	3145	CB ALA A 520	73.427	5.513	41.206	1.00 18.41

3146	N	TYR	A	521	71.811	3.561	43.410	1.00	17.07	3191	OE1	GLU	A	526	84.455	-2.518	44.447	1.00	18.35
3147	CA	TYR	A	521	70.819	3.494	44.486	1.00	16.73	3192	OE2	GLU	A	526	84.830	-0.361	44.367	1.00	20.55
3148	C	TYR	A	521	71.260	2.579	45.612	1.00	17.27	3193	N	GLY	A	527	80.932	-4.816	44.303	1.00	16.41
3149	O	TYR	A	521	70.528	2.470	46.610	1.00	17.61	3194	CA	GLY	A	527	80.349	-6.100	44.587	1.00	18.62
3150	CB	TYR	A	521	69.446	3.021	43.941	1.00	17.24	3195	C	GLY	A	527	78.868	-6.310	44.654	1.00	19.21
3151	CG	TYR	A	521	68.942	3.859	42.764	1.00	15.38	3196	O	GLY	A	527	78.114	-5.715	43.903	1.00	19.86
3152	CD1	TYR	A	521	69.117	5.247	42.743	1.00	15.18	3197	N	THR	A	528	78.364	-7.119	45.605	1.00	20.27
3153	CD2	TYR	A	521	68.284	3.264	41.724	1.00	15.31	3198	CA	THR	A	528	76.950	-7.510	45.574	1.00	18.39
3154	CE1	TYR	A	521	68.738	6.002	41.655	1.00	16.88	3199	C	THR	A	528	76.092	-6.707	46.515	1.00	19.42
3155	CE2	TYR	A	521	67.798	4.003	40.641	1.00	16.48	3200	O	THR	A	528	74.938	-7.063	46.774	1.00	18.50
3156	CZ	TYR	A	521	68.057	5.367	40.617	1.00	17.62	3201	CB	THR	A	528	76.855	-9.024	45.904	1.00	18.15
3157	OH	TYR	A	521	67.606	6.097	39.531	1.00	19.26	3202	OG1	THR	A	528	77.414	-9.233	47.211	1.00	20.44
3158	N	ALA	A	522	72.417	1.907	45.435	1.00	17.17	3203	CG2	THR	A	528	77.688	-9.855	44.941	1.00	17.77
3159	CA	ALA	A	522	72.945	1.042	46.518	1.00	15.89	3204	N	ALA	A	529	76.662	-5.642	47.063	1.00	18.16
3160	C	ALA	A	522	73.921	1.876	47.348	1.00	15.60	3205	CA	ALA	A	529	75.933	-4.712	47.906	1.00	18.05
3161	O	ALA	A	522	74.342	2.981	46.946	1.00	17.19	3206	C	ALA	A	529	74.630	-4.330	47.203	1.00	18.52
3162	CB	ALA	A	522	73.659	-0.164	45.905	1.00	13.85	3207	O	ALA	A	529	73.580	-4.348	47.859	1.00	16.31
3163	N	THR	A	523	74.102	1.561	48.625	1.00	15.78	3208	CB	ALA	A	529	76.703	-3.413	48.157	1.00	18.09
3164	CA	THR	A	523	75.072	2.230	49.489	1.00	17.82	3209	N	ARG	A	530	74.624	-4.063	45.907	1.00	17.37
3165	C	THR	A	523	76.470	1.956	48.944	1.00	18.92	3210	CA	ARG	A	530	73.422	-3.669	45.184	1.00	16.22
3166	O	THR	A	523	77.211	2.947	49.304	1.00	17.26	3211	C	ARG	A	530	72.334	-4.739	45.116	1.00	16.28
3167	CB	THR	A	523	74.948	1.890	50.976	1.00	17.94	3212	O	ARG	A	530	71.148	-4.377	45.045	1.00	15.45
3168	OG1	THR	A	523	75.385	0.524	51.116	1.00	17.69	3213	CB	ARG	A	530	73.783	-3.225	43.762	1.00	15.05
3169	CG2	THR	A	523	73.506	2.011	51.516	1.00	16.78	3214	CG	ARG	A	530	74.440	-4.346	42.940	1.00	16.74
3170	N	THR	A	524	76.940	1.218	48.019	1.00	16.59	3215	CD	ARG	A	530	74.961	-3.751	41.630	1.00	14.90
3171	CA	THR	A	524	78.214	1.239	47.375	1.00	17.47	3216	NE	ARG	A	530	76.197	-2.937	41.763	1.00	15.63
3172	C	THR	A	524	77.987	0.549	46.014	1.00	15.97	3217	CZ	ARG	A	530	76.515	-2.064	40.802	1.00	15.30
3173	O	THR	A	524	77.245	-0.434	46.035	1.00	15.00	3218	NH1	ARG	A	530	77.670	-1.407	40.853	1.00	17.75
3174	CB	THR	A	524	79.381	0.537	48.089	1.00	16.77	3219	NH2	ARG	A	530	75.706	-1.836	39.773	1.00	12.09
3175	OG1	THR	A	524	80.598	0.447	47.315	1.00	18.09	3220	N	ILE	A	531	72.700	-6.005	45.108	1.00	14.54
3176	CG2	THR	A	524	79.009	-0.895	48.485	1.00	17.48	3221	CA	ILE	A	531	71.804	-7.113	45.021	1.00	17.37
3177	N	PRO	A	525	78.671	0.941	44.975	1.00	16.83	3222	C	ILE	A	531	71.001	-7.347	46.318	1.00	18.65
3178	CA	PRO	A	525	78.667	0.231	43.696	1.00	16.43	3223	O	ILE	A	531	69.754	-7.487	46.311	1.00	14.76
3179	C	PRO	A	525	79.532	-1.019	43.697	1.00	17.20	3224	CB	ILE	A	531	72.556	-8.391	44.601	1.00	17.38
3180	O	PRO	A	525	79.479	-1.868	42.773	1.00	16.05	3225	CG1	ILE	A	531	73.146	-8.298	43.182	1.00	17.59
3181	CB	PRO	A	525	79.261	1.241	42.734	1.00	17.75	3226	CG2	ILE	A	531	71.624	-9.601	44.601	1.00	16.93
3182	CG	PRO	A	525	80.236	2.061	43.551	1.00	17.07	3227	CD1	ILE	A	531	73.965	-9.553	42.804	1.00	16.77
3183	CD	PRO	A	525	79.581	2.153	44.935	1.00	16.46	3228	N	THR	A	532	71.717	-7.408	47.426	1.00	16.30
3184	N	GLU	A	526	80.334	-1.296	44.754	1.00	17.68	3229	CA	THR	A	532	71.120	-7.596	48.745	1.00	17.14
3185	CA	GLU	A	526	81.242	-2.413	44.797	1.00	15.57	3230	C	THR	A	532	70.203	-6.408	49.093	1.00	16.96
3186	C	GLU	A	526	80.552	-3.755	45.025	1.00	18.65	3231	O	THR	A	532	69.122	-6.670	49.634	1.00	17.94
3187	O	GLU	A	526	79.678	-3.828	45.910	1.00	17.57	3232	CB	THR	A	532	72.202	-7.696	49.838	1.00	18.30
3188	CB	GLU	A	526	82.241	-2.286	45.993	1.00	18.74	3233	OG1	THR	A	532	73.048	-8.840	49.519	1.00	17.90
3189	CG	GLU	A	526	83.196	-1.098	45.920	1.00	17.93	3234	CG2	THR	A	532	71.578	-7.989	51.205	1.00	15.71
3190	CD	GLU	A	526	84.240	-1.354	44.831	1.00	20.14	3235	N	GLU	A	533	70.608	-5.180	48.808	1.00	13.67

3236	CA	GLU A 533	69.821	-3.993	49.110	1.00 15.12	3281	O	ILE A 538	59.479	-6.811	49.400	1.00 16.47
3237	C	GLU A 533	68.532	-3.891	48.317	1.00 16.63	3282	CB	ILE A 538	61.777	-6.836	46.920	1.00 16.94
3238	O	GLU A 533	67.551	-3.400	48.903	1.00 14.08	3283	CG1	ILE A 538	62.083	-5.982	45.686	1.00 14.36
3239	CB	GLU A 533	70.707	-2.740	49.008	1.00 16.01	3284	CG2	ILE A 538	60.667	-7.886	46.675	1.00 17.13
3240	CG	GLU A 533	71.682	-2.653	50.183	1.00 17.57	3285	CD1	ILE A 538	62.805	-6.628	44.509	1.00 13.95
3241	CD	GLU A 533	72.716	-1.580	50.093	1.00 19.20	3286	N	GLN A 539	61.538	-7.186	50.141	1.00 16.57
3242	OE1	GLU A 533	73.811	-1.717	50.714	1.00 21.48	3287	CA	GLN A 539	61.128	-7.943	51.314	1.00 17.53
3243	OE2	GLU A 533	72.475	-0.536	49.428	1.00 20.43	3288	C	GLN A 539	60.345	-7.077	52.312	1.00 18.11
3244	N	LEU A 534	68.465	-4.294	47.052	1.00 14.75	3289	O	GLN A 539	59.366	-7.553	52.893	1.00 17.99
3245	CA	LEU A 534	67.179	-4.230	46.320	1.00 14.76	3290	CB	GLN A 539	62.351	-8.523	52.027	1.00 19.31
3246	C	LEU A 534	66.255	-5.331	46.838	1.00 13.97	3291	CG	GLN A 539	62.149	-9.256	53.324	1.00 19.71
3247	O	LEU A 534	65.040	-5.162	46.998	1.00 13.22	3292	CD	GLN A 539	63.417	-9.837	53.936	1.00 20.54
3248	CB	LEU A 534	67.451	-4.277	44.804	1.00 11.25	3293	OE1	GLN A 539	64.431	-9.149	54.033	1.00 22.88
3249	CG	LEU A 534	66.205	-4.408	43.904	1.00 13.31	3294	NE2	GLN A 539	63.404	-11.074	54.356	1.00 19.77
3250	CD1	LEU A 534	65.165	-3.291	44.168	1.00 10.17	3295	N	SER A 540	60.765	-5.844	52.489	1.00 18.42
3251	CD2	LEU A 534	66.721	-4.308	42.454	1.00 10.59	3296	CA	SER A 540	60.102	-4.916	53.403	1.00 20.34
3252	N	LYS A 535	66.805	-6.516	47.087	1.00 13.87	3297	C	SER A 540	58.723	-4.480	52.906	1.00 20.30
3253	CA	LYS A 535	66.086	-7.618	47.715	1.00 15.88	3298	O	SER A 540	57.763	-4.529	53.714	1.00 16.87
3254	C	LYS A 535	65.530	-7.196	49.082	1.00 16.79	3299	CB	SER A 540	61.125	-3.801	53.586	1.00 21.39
3255	O	LYS A 535	64.377	-7.547	49.376	1.00 17.52	3300	CG	SER A 540	60.542	-2.651	54.113	1.00 26.78
3256	CB	LYS A 535	66.887	-8.917	47.860	1.00 15.40	3301	N	LEU A 541	58.502	-4.242	51.613	1.00 17.30
3257	CG	LYS A 535	67.402	-9.601	46.617	1.00 18.60	3302	CA	LEU A 541	57.127	-3.909	51.140	1.00 18.58
3258	CD	LYS A 535	68.119	-10.918	46.903	1.00 17.82	3303	C	LEU A 541	56.231	-5.132	51.270	1.00 18.04
3259	CE	LYS A 535	68.558	-11.541	45.575	1.00 18.33	3304	O	LEU A 541	55.047	-5.034	51.690	1.00 17.70
3260	NZ	LYS A 535	59.546	-12.644	45.766	1.00 16.36	3305	CB	LEU A 541	57.128	-3.311	49.731	1.00 19.55
3261	N	GLN A 536	66.207	-6.389	49.915	1.00 16.15	3306	CG	LEU A 541	57.908	-2.022	49.522	1.00 20.99
3262	CA	GLN A 536	65.663	-5.931	51.188	1.00 17.43	3307	CD1	LEU A 541	58.100	-1.486	48.104	1.00 20.76
3263	C	GLN A 536	64.484	-4.948	51.011	1.00 15.85	3308	CD2	LEU A 541	57.190	-0.836	50.210	1.00 21.46
3264	O	GLN A 536	63.556	-4.932	51.829	1.00 13.29	3309	N	HIS A 542	56.739	-6.322	50.902	1.00 15.72
3265	CB	GLN A 536	66.735	-5.260	52.068	1.00 16.73	3310	CA	HIS A 542	55.993	-7.545	50.990	1.00 17.12
3266	CG	GLN A 536	67.783	-6.230	52.583	1.00 20.31	3311	C	HIS A 542	55.499	-7.790	52.421	1.00 20.37
3267	CD	GLN A 536	68.982	-5.556	53.221	1.00 22.94	3312	O	HIS A 542	54.326	-8.187	52.598	1.00 17.99
3268	OE1	GLN A 536	69.836	-4.925	52.614	1.00 21.17	3313	CB	HIS A 542	56.747	-8.783	50.476	1.00 17.02
3270	N	LEU A 537	64.505	-4.105	49.992	1.00 16.38	3314	CG	HIS A 542	56.882	-8.831	48.975	1.00 16.64
3271	CA	LEU A 537	63.425	-3.174	49.650	1.00 16.60	3315	ND1	HIS A 542	57.700	-9.780	48.377	1.00 15.29
3272	C	LEU A 537	62.179	-4.051	49.336	1.00 17.04	3316	CD2	HIS A 542	56.349	-8.154	47.933	1.00 14.04
3273	O	LEU A 537	61.080	-3.702	49.797	1.00 16.16	3317	CE1	HIS A 542	57.670	-9.669	47.055	1.00 15.74
3274	CB	LEU A 537	63.756	-2.314	48.435	1.00 17.59	3318	NE2	HIS A 542	56.848	-8.690	46.754	1.00 14.08
3275	CG	LEU A 537	62.757	-1.314	47.829	1.00 15.05	3319	N	GLN A 543	56.340	-7.489	53.425	1.00 19.61
3276	CD1	LEU A 537	63.348	-0.200	46.975	1.00 16.00	3320	CA	GLN A 543	55.955	-7.702	54.817	1.00 22.30
3277	CD2	LEU A 537	61.771	-2.134	46.970	1.00 15.65	3321	C	GLN A 543	54.786	-6.794	55.164	1.00 22.43
3278	N	ILE A 538	62.361	-5.013	48.468	1.00 16.09	3322	O	GLN A 543	54.023	-7.124	56.093	1.00 20.41
3279	CA	ILE A 538	61.288	-5.922	48.067	1.00 16.51	3323	CB	GLN A 543	57.132	-7.462	55.797	1.00 23.32
3280	C	ILE A 538	60.701	-6.677	49.245	1.00 17.89	3324	CG	GLN A 543	58.247	-8.469	55.718	1.00 26.39
							3325	CD	GLN A 543	59.583	-8.082	56.334	1.00 29.94

3326	OE1 GLN A 543	60.499	-8.911	56.516	1.00 29.73	3371	CB ASN A 549	54.882	-3.275	39.173	1.00 14.17
3327	NE2 GLN A 543	59.764	-6.816	56.705	1.00 28.77	3372	CG ASN A 549	53.592	-4.005	39.512	1.00 15.52
3328	N GLN A 544	54.621	-5.649	54.503	1.00 21.34	3373	OD1 ASN A 549	53.667	-5.127	40.037	1.00 15.71
3329	CA GLN A 544	53.444	-4.814	54.771	1.00 24.96	3374	ND2 ASN A 549	52.374	-3.530	39.214	1.00 11.04
3330	C GLN A 544	52.339	-5.016	53.751	1.00 23.83	3375	N MET A 550	58.240	-3.755	38.342	1.00 14.17
3331	O GLN A 544	51.495	-4.154	53.542	1.00 23.04	3376	CA MET A 550	59.397	-3.031	37.813	1.00 14.20
3332	CB GLN A 544	53.875	-3.348	54.782	1.00 29.05	3377	C MET A 550	59.099	-2.392	36.448	1.00 14.75
3333	CG GLN A 544	54.974	-3.219	55.851	1.00 34.54	3378	O MET A 550	58.661	-3.107	35.535	1.00 12.87
3334	CD GLN A 544	54.552	-3.697	57.224	1.00 37.02	3379	CB MET A 550	60.626	-3.948	37.655	1.00 13.94
3335	OE1 GLN A 544	53.442	-3.372	57.648	1.00 39.96	3380	CG MET A 550	61.452	-4.226	38.909	1.00 15.03
3336	NE2 GLN A 544	55.388	-4.465	57.921	1.00 38.54	3381	SD MET A 550	62.697	-5.561	38.695	1.00 14.47
3337	N ARG A 545	52.376	-6.121	53.023	1.00 24.22	3382	CB MET A 550	63.764	-4.727	37.472	1.00 16.01
3338	CA ARG A 545	51.393	-6.420	51.983	1.00 26.56	3383	ASP A 551	59.368	-1.092	36.301	1.00 13.68
3339	C ARG A 545	51.405	-5.479	50.781	1.00 22.89	3384	CA ASP A 551	59.392	-0.396	35.011	1.00 14.18
3340	O ARG A 545	50.354	-5.136	50.220	1.00 20.28	3385	C ASP A 551	60.610	-0.949	34.274	1.00 15.34
3341	CB ARG A 545	49.970	-6.500	52.565	1.00 32.05	3386	O ASP A 551	61.711	-0.908	34.871	1.00 16.12
3342	CG ARG A 545	49.843	-7.658	53.558	1.00 38.97	3387	CB ASP A 551	59.565	1.119	35.255	1.00 13.46
3343	CD ARG A 545	48.545	-8.386	53.314	1.00 45.28	3388	CG ASP A 551	59.452	1.990	34.034	1.00 14.83
3344	NE ARG A 545	47.466	-8.211	54.228	1.00 50.20	3389	OD1 ASP A 551	59.595	1.439	32.872	1.00 16.30
3345	CZ ARG A 545	46.728	-7.225	54.696	1.00 52.67	3390	OD2 ASP A 551	59.255	3.209	34.103	1.00 12.40
3346	NH1 ARG A 545	46.938	-5.972	54.297	1.00 54.30	3391	N VAL A 552	60.530	-1.561	33.107	1.00 15.18
3347	NH2 ARG A 545	45.760	-7.508	55.581	1.00 52.76	3392	CA VAL A 552	61.659	-2.143	32.393	1.00 14.43
3348	N ILE A 546	52.568	-4.974	50.391	1.00 19.58	3393	C VAL A 552	61.698	-1.675	30.951	1.00 14.19
3349	CA ILE A 546	52.691	-4.154	49.197	1.00 18.16	3394	O VAL A 552	60.693	-1.489	30.256	1.00 15.99
3350	C ILE A 546	53.570	-4.849	48.165	1.00 17.48	3395	CB VAL A 552	61.674	-3.691	32.386	1.00 14.09
3351	O ILE A 546	54.622	-5.411	48.473	1.00 13.86	3396	CG1 VAL A 552	62.001	-4.194	33.795	1.00 11.24
3352	CB ILE A 546	53.198	-2.730	49.501	1.00 18.44	3397	CG2 VAL A 552	60.321	-4.237	31.901	1.00 11.60
3353	CG1 ILE A 546	52.267	-2.011	50.485	1.00 18.83	3398	N VAL A 553	62.900	-1.482	30.427	1.00 13.93
3354	CG2 ILE A 546	53.319	-1.850	48.254	1.00 16.84	3399	CA VAL A 553	63.153	-0.895	29.128	1.00 15.34
3355	CD1 ILE A 546	52.910	-0.740	51.046	1.00 20.08	3400	C VAL A 553	63.848	-1.812	28.140	1.00 18.26
3356	N GLY A 547	53.077	-4.958	46.936	1.00 16.21	3401	O VAL A 553	64.912	-1.514	27.574	1.00 18.77
3357	CA GLY A 547	53.802	-5.583	45.845	1.00 13.51	3402	CB VAL A 553	63.939	0.406	29.373	1.00 14.83
3358	C GLY A 547	54.760	-4.619	45.151	1.00 14.12	3403	CG1 VAL A 553	64.111	1.249	28.108	1.00 17.28
3359	O GLY A 547	54.720	-3.383	45.292	1.00 12.19	3404	CG2 VAL A 553	63.326	1.232	30.565	1.00 16.73
3360	N VAL A 548	55.614	-5.196	44.275	1.00 11.18	3405	N TYR A 554	63.251	-2.945	27.782	1.00 19.23
3361	CA VAL A 548	56.557	-4.349	43.534	1.00 11.75	3406	CA TYR A 554	63.787	-3.864	26.789	1.00 17.41
3362	C VAL A 548	56.468	-4.574	42.042	1.00 12.64	3407	C TYR A 554	63.647	-3.343	25.367	1.00 17.63
3363	O VAL A 548	56.761	-5.829	41.654	1.00 11.59	3408	O TYR A 554	64.113	-4.065	24.465	1.00 18.06
3364	CB VAL A 548	57.995	-4.621	43.998	1.00 13.98	3409	CB TYR A 554	63.080	-5.237	26.873	1.00 17.61
3365	CG1 VAL A 548	58.998	-3.860	43.135	1.00 15.29	3410	CG TYR A 554	63.378	-5.873	28.232	1.00 16.57
3366	CG2 VAL A 548	58.278	-4.241	45.466	1.00 12.74	3411	CD1 TYR A 554	64.653	-6.384	28.473	1.00 17.67
3367	N ASN A 549	56.225	-3.678	41.208	1.00 12.65	3412	CD2 TYR A 554	62.423	-5.941	29.222	1.00 16.40
3368	CA ASN A 549	56.184	-3.878	39.757	1.00 13.79	3413	CE1 TYR A 554	64.985	-6.939	29.706	1.00 17.79
3369	C ASN A 549	57.405	-3.147	39.191	1.00 15.40	3414	CE2 TYR A 554	62.717	-6.544	30.457	1.00 17.52
3370	O ASN A 549	57.639	-1.977	39.536	1 00 14.02	3415	CZ TYR A 554	64.006	-7.002	30.692	1.00 17.50

3596	CB	ARG A 575	64.798	-3.050	14.073	1.00	15.06	3641	CG	ASN A 581	70.979	4.271	7.815	1.00	24.55
3597	CG	ARG A 575	63.996	-3.916	15.070	1.00	15.86	3642	OD1	ASN A 581	72.201	4.336	7.991	1.00	25.71
3598	CD	ARG A 575	62.468	-3.788	14.682	1.00	16.08	3643	ND2	ASN A 581	70.436	4.847	6.760	1.00	22.88
3599	NE	ARG A 575	61.750	-4.691	15.785	1.00	13.65	3644	N	TYR A 582	70.211	1.744	11.428	1.00	18.90
3600	CZ	ARG A 575	61.087	-4.506	16.914	1.00	16.15	3645	CA	TYR A 582	69.377	1.345	12.592	1.00	20.45
3601	NH1	ARG A 575	60.840	-3.302	17.495	1.00	13.01	3646	C	TYR A 582	68.045	2.071	12.591	1.00	18.67
3602	NH2	ARG A 575	60.591	-5.606	17.516	1.00	11.72	3647	O	TYR A 582	68.050	3.319	12.396	1.00	17.45
3603	N	THR A 576	67.240	-3.018	11.669	1.00	17.48	3648	CB	TYR A 582	70.093	1.730	13.900	1.00	21.60
3604	CA	THR A 576	67.911	-2.206	10.648	1.00	16.92	3649	CG	TYR A 582	71.394	0.997	14.143	1.00	26.25
3605	C	THR A 576	67.062	-2.149	9.365	1.00	18.54	3650	CD1	TYR A 582	72.639	1.501	13.726	1.00	27.97
3606	O	THR A 576	66.283	-3.087	9.134	1.00	19.15	3651	CD2	TYR A 582	71.374	-0.230	14.777	1.00	27.31
3607	CB	THR A 576	69.304	-2.708	10.228	1.00	17.51	3652	CE1	TYR A 582	73.853	0.831	13.960	1.00	28.48
3608	OG1	THR A 576	69.224	-4.053	9.768	1.00	12.75	3653	CE2	TYR A 582	72.561	-0.924	15.000	1.00	28.99
3609	CG2	THR A 576	70.351	-2.561	11.345	1.00	18.13	3654	CZ	TYR A 582	73.774	-0.390	14.589	1.00	28.99
3610	N	ASP A 577	67.206	-1.088	8.567	1.00	18.10	3655	OH	TYR A 582	74.899	-1.115	14.864	1.00	18.57
3611	CA	ASP A 577	66.406	-0.999	7.351	1.00	18.80	3656	N	THR A 583	66.912	1.437	12.737	1.00	18.57
3612	C	ASP A 577	67.218	-1.512	6.154	1.00	20.47	3657	CA	THR A 583	65.623	2.143	12.764	1.00	19.17
3613	O	ASP A 577	68.348	-2.037	6.306	1.00	22.66	3658	C	THR A 583	65.399	2.672	14.204	1.00	19.21
3614	CB	ASP A 577	65.858	0.404	7.051	1.00	18.16	3659	O	THR A 583	66.002	2.240	15.227	1.00	15.73
3615	CG	ASP A 577	66.941	1.424	6.856	1.00	19.10	3660	CB	THR A 583	64.442	1.271	12.295	1.00	21.01
3616	OD1	ASP A 577	66.636	2.634	7.169	1.00	19.08	3661	OG1	THR A 583	64.334	0.091	13.179	1.00	19.15
3617	OD2	ASP A 577	68.119	1.198	6.485	1.00	16.70	3662	CG2	THR A 583	64.598	0.758	10.847	1.00	20.19
3618	N	SER A 578	66.674	-1.364	4.963	1.00	20.77	3663	N	ASN A 584	64.574	3.728	14.303	1.00	16.30
3619	CA	SER A 578	67.276	-1.837	3.705	1.00	21.43	3664	CA	ASN A 584	64.420	4.507	15.514	1.00	17.48
3620	C	SER A 578	68.503	-1.061	3.308	1.00	21.24	3665	C	ASN A 584	63.063	4.434	16.164	1.00	17.05
3621	O	SER A 578	69.334	-1.575	2.544	1.00	21.58	3666	O	ASN A 584	62.469	5.447	16.559	1.00	16.19
3622	CB	SER A 578	66.212	-1.815	2.599	1.00	23.81	3667	CB	ASN A 584	64.779	5.966	15.133	1.00	19.28
3623	OG	SER A 578	65.419	-2.993	2.665	1.00	24.09	3668	CG	ASN A 584	65.141	6.823	16.319	1.00	20.58
3624	N	ASN A 579	68.692	0.150	3.800	1.00	21.04	3669	OD1	ASN A 584	65.304	6.339	17.435	1.00	22.86
3625	CA	ASN A 579	69.893	0.918	3.551	1.00	22.84	3670	ND2	ASN A 584	65.101	8.148	16.199	1.00	22.27
3626	C	ASN A 579	71.069	0.581	4.470	1.00	22.28	3671	N	GLY A 585	62.499	3.249	16.338	1.00	17.36
3627	O	ASN A 579	72.244	1.070	4.370	1.00	22.77	3672	CA	GLY A 585	61.169	3.095	16.940	1.00	18.20
3628	CB	ASN A 579	69.572	2.403	3.670	1.00	24.77	3673	C	GLY A 585	61.073	3.688	18.348	1.00	19.43
3629	CG	ASN A 579	68.611	2.929	2.641	1.00	27.96	3674	O	GLY A 585	60.000	4.151	18.739	1.00	17.42
3630	OD1	ASN A 579	67.940	3.947	2.900	1.00	30.34	3675	N	SER A 586	62.149	3.685	19.128	1.00	20.93
3631	ND2	ASN A 579	68.431	2.198	1.548	1.00	27.67	3676	CA	SER A 586	62.095	4.195	20.490	1.00	21.54
3632	N	GLY A 580	70.811	-0.191	5.501	1.00	21.69	3677	C	SER A 586	62.259	5.711	20.590	1.00	20.81
3633	CA	GLY A 580	71.749	-0.563	6.551	1.00	20.67	3678	O	SER A 586	61.993	6.277	21.652	1.00	20.13
3634	C	GLY A 580	71.708	0.335	7.781	1.00	20.28	3679	CB	SER A 586	63.221	3.538	21.302	1.00	20.63
3635	O	GLY A 580	72.723	0.373	8.505	1.00	20.34	3680	OG	SER A 586	64.491	4.039	20.860	1.00	21.23
3636	N	ASN A 581	70.727	1.230	7.907	1.00	19.77	3681	N	GLY A 587	62.771	6.354	19.558	1.00	19.63
3637	CA	ASN A 581	70.647	2.096	9.057	1.00	20.14	3682	CA	GLY A 587	63.102	7.781	19.629	1.00	20.56
3638	C	ASN A 581	69.811	1.448	10.186	1.00	20.05	3683	C	GLY A 587	64.469	8.006	20.279	1.00	21.87
3639	O	ASN A 581	68.809	0.802	9.843	1.00	20.06	3684	O	GLY A 587	64.930	9.158	20.346	1.00	21.43
3640	CB	ASN A 581	70.061	3.486	8.758	1.00	20.77	3685	N	CYS A 588	65.213	6.945	20.630	1.00	19.06

3686	CA	CYS A 588	66.495	7.043	21.300	1.00	19.09	3731	O	THR A 594	61.673	-11.162	18.635	1.00	16.76
3687	C	CYS A 588	67.651	6.569	20.417	1.00	20.16	3732	CB	THR A 594	61.234	-8.677	20.250	1.00	15.31
3688	O	CYS A 588	68.797	6.442	20.864	1.00	18.88	3733	CG1	THR A 594	60.306	-7.885	19.481	1.00	16.09
3689	CB	CYS A 588	66.462	6.167	22.569	1.00	18.06	3734	CG2	THR A 594	61.715	-7.890	21.453	1.00	15.49
3690	SG	CYS A 588	65.249	6.772	23.792	1.00	20.94	3735	N	GLU A 595	61.862	-9.680	16.956	1.00	17.58
3691	CA	GLY A 589	67.358	6.343	19.130	1.00	19.74	3736	CA	GLU A 595	61.519	-10.670	15.952	1.00	17.42
3692	N	GLY A 589	68.464	5.999	18.224	1.00	20.77	3737	C	GLU A 595	62.715	-11.589	15.648	1.00	18.14
3693	C	GLY A 589	68.511	4.521	17.843	1.00	20.75	3738	O	GLU A 595	62.627	-12.532	14.859	1.00	19.18
3694	O	GLY A 589	69.319	4.222	16.957	1.00	21.38	3739	CB	GLU A 595	60.966	-10.097	14.646	1.00	18.92
3695	N	ASN A 590	67.768	3.611	18.454	1.00	18.78	3740	CG	GLU A 595	61.955	-9.284	13.797	1.00	17.41
3696	CA	ASN A 590	67.823	2.183	18.077	1.00	17.60	3741	CD	GLU A 595	62.217	-7.889	14.333	1.00	18.02
3697	C	ASN A 590	66.576	1.529	18.652	1.00	17.96	3742	OB1	GLU A 595	61.964	-7.461	15.493	1.00	16.28
3698	O	ASN A 590	65.865	2.190	19.463	1.00	17.56	3743	OB2	GLU A 595	62.768	-7.075	13.557	1.00	18.81
3699	CB	ASN A 590	69.087	1.484	18.624	1.00	15.88	3744	N	HIS A 596	63.900	-11.351	16.189	1.00	16.45
3700	CG	ASN A 590	69.144	1.355	20.139	1.00	17.35	3745	CA	HIS A 596	65.050	-12.239	15.996	1.00	15.59
3701	OD1	ASN A 590	68.469	0.536	20.774	1.00	15.30	3746	C	HIS A 596	65.076	-13.182	17.190	1.00	16.08
3702	ND2	ASN A 590	69.897	2.207	20.808	1.00	15.71	3747	O	HIS A 596	65.031	-12.701	18.324	1.00	15.72
3703	N	GLU A 591	66.335	0.275	18.302	1.00	17.77	3748	CB	HIS A 596	66.324	-11.404	15.934	1.00	14.25
3704	CA	GLU A 591	65.200	-0.435	18.873	1.00	18.01	3749	CG	HIS A 596	66.598	-10.769	14.592	1.00	16.18
3705	C	GLU A 591	65.575	-1.923	18.828	1.00	18.01	3750	ND1	HIS A 596	67.579	-9.788	14.434	1.00	14.53
3706	O	GLU A 591	66.264	-2.419	17.909	1.00	17.69	3751	CD2	HIS A 596	66.014	-10.918	13.388	1.00	13.81
3707	CB	GLU A 591	63.831	-0.072	18.251	1.00	19.26	3752	CE1	HIS A 596	67.617	-9.420	13.163	1.00	15.09
3708	CG	GLU A 591	63.658	-0.382	16.805	1.00	18.33	3753	NE2	HIS A 596	66.708	-10.116	12.524	1.00	15.29
3709	CD	GLU A 591	62.322	-0.090	16.134	1.00	19.76	3754	N	PRO A 597	64.965	-14.485	16.976	1.00	16.49
3710	OE1	GLU A 591	62.383	0.617	15.092	1.00	18.91	3755	CA	PRO A 597	64.763	-15.436	18.023	1.00	17.55
3711	OE2	GLU A 591	61.249	-0.589	16.551	1.00	18.16	3756	C	PRO A 597	65.654	-15.307	19.250	1.00	18.38
3712	N	PHE A 592	65.262	-2.635	19.900	1.00	15.35	3757	O	PRO A 597	65.097	-15.446	20.358	1.00	17.58
3713	CA	PHE A 592	65.646	-4.041	20.070	1.00	18.51	3758	CB	PRO A 597	64.928	-16.799	17.319	1.00	17.50
3714	C	PHE A 592	64.787	-4.958	19.219	1.00	16.58	3759	CG	PRO A 597	64.306	-16.514	15.953	1.00	18.51
3715	O	PHE A 592	63.532	-4.916	19.203	1.00	18.31	3760	CD	PRO A 597	64.817	-15.129	15.637	1.00	18.53
3716	CB	PHE A 592	65.507	-4.390	21.572	1.00	18.66	3761	N	MET A 598	66.964	-15.173	19.087	1.00	15.98
3717	CG	PHE A 592	66.320	-5.575	22.007	1.00	19.55	3762	CA	MET A 598	67.874	-15.133	20.231	1.00	15.82
3718	CD1	PHE A 592	67.687	-5.484	22.227	1.00	21.67	3763	C	MET A 598	67.729	-13.791	20.940	1.00	15.34
3719	CD2	PHE A 592	65.700	-6.800	22.204	1.00	21.14	3764	O	MET A 598	68.082	-13.708	22.130	1.00	16.95
3720	CR1	PHE A 592	68.400	-6.593	22.666	1.00	21.13	3765	CB	MET A 598	69.336	-15.412	19.803	1.00	16.00
3721	CE2	PHE A 592	66.399	-7.894	22.657	1.00	21.68	3766	CG	MET A 598	69.574	-16.841	19.325	1.00	13.68
3722	CZ	PHE A 592	67.750	-7.786	22.877	1.00	20.22	3767	SD	MET A 598	69.207	-18.085	20.579	1.00	13.98
3723	N	ALA A 593	65.422	-5.805	18.433	1.00	15.23	3768	CE	MET A 598	70.593	-17.828	21.697	1.00	15.11
3724	CA	ALA A 593	64.731	-6.643	17.459	1.00	14.58	3769	N	ALA A 599	67.344	-12.740	20.202	1.00	14.72
3725	C	ALA A 593	64.218	-7.941	18.052	1.00	15.78	3770	CA	ALA A 599	67.059	-11.481	20.876	1.00	15.20
3726	O	ALA A 593	64.818	-8.986	17.839	1.00	15.37	3771	C	ALA A 599	65.783	-11.665	21.708	1.00	16.47
3727	CB	ALA A 593	65.653	-6.921	16.263	1.00	14.49	3772	O	ALA A 599	65.749	-11.281	22.874	1.00	17.10
3728	N	THR A 594	63.084	-7.909	18.737	1.00	13.64	3773	CB	ALA A 599	66.943	-10.328	19.898	1.00	13.55
3729	CA	THR A 594	62.430	-9.049	19.319	1.00	17.21	3774	N	GLN A 600	64.731	-12.308	21.178	1.00	16.72
3730	C	THR A 594	61.898	-10.007	18.255	1.00	18.41	3775	CA	GLN A 600	63.525	-12.575	21.946	1.00	18.51

3776	C	GLN A 600	63.860	-13.406	23.201	1.00	17.76	3821	O	ASP A 605	65.426	-14.517	32.390	1.00	15.93
3777	O	GLN A 600	63.429	-13.048	24.311	1.00	13.69	3822	CB	ASP A 605	66.722	-15.477	29.523	1.00	14.57
3778	CB	GLN A 600	62.404	-13.240	21.137	1.00	17.71	3823	CG	ASP A 605	66.881	-16.749	28.698	1.00	18.15
3779	CG	GLN A 600	61.117	-13.534	21.935	1.00	16.56	3824	OD1	ASP A 605	67.938	-16.953	28.012	1.00	14.80
3780	CD	GLN A 600	60.174	-14.357	21.052	1.00	16.99	3825	OD2	ASP A 605	65.927	-17.564	28.720	1.00	15.40
3781	OE1	GLN A 600	60.365	-15.573	20.886	1.00	17.99	3826	N	SER A 606	65.555	-12.903	30.809	1.00	15.59
3782	NE2	GLN A 600	59.183	-13.690	20.475	1.00	12.76	3827	CA	SER A 606	65.716	-11.772	31.721	1.00	14.83
3783	N	LYS A 601	64.723	-14.418	23.042	1.00	17.63	3828	C	SER A 606	64.501	-11.560	32.614	1.00	14.39
3784	CA	LYS A 601	65.138	-15.279	24.130	1.00	17.70	3829	O	SER A 606	64.675	-11.460	33.840	1.00	13.45
3785	C	LYS A 601	65.881	-14.491	25.221	1.00	18.25	3830	CB	SER A 606	66.094	-10.483	30.977	1.00	14.58
3786	O	LYS A 601	65.662	-14.783	26.399	1.00	16.32	3831	OG	SER A 606	66.281	-9.390	31.898	1.00	14.28
3787	CB	LYS A 601	66.023	-16.457	23.633	1.00	18.32	3832	N	VAL A 607	63.265	-11.480	32.095	1.00	14.64
3788	CG	LYS A 601	66.619	-17.286	24.778	1.00	17.88	3833	CA	VAL A 607	62.127	-11.281	33.004	1.00	15.38
3789	CD	LYS A 601	67.393	-18.512	24.279	1.00	18.60	3834	C	VAL A 607	61.945	-12.521	33.896	1.00	15.96
3790	CE	LYS A 601	68.237	-19.167	25.397	1.00	18.85	3835	O	VAL A 607	61.514	-12.318	35.035	1.00	15.28
3791	NZ	LYS A 601	67.398	-19.618	26.571	1.00	16.70	3836	CB	VAL A 607	60.810	-10.937	32.280	1.00	15.47
3792	N	PHE A 602	66.732	-13.517	24.854	1.00	17.63	3837	CG1	VAL A 607	60.974	-9.551	31.618	1.00	13.07
3793	CA	PHE A 602	66.730	-12.649	25.854	1.00	16.13	3838	CG2	VAL A 607	60.425	-12.035	31.284	1.00	12.85
3794	C	PHE A 602	66.329	-12.012	26.764	1.00	16.27	3839	N	ASN A 608	62.193	-13.746	33.446	1.00	14.92
3795	O	PHE A 602	66.554	-11.907	28.009	1.00	14.81	3840	CA	ASN A 608	62.161	-14.916	34.299	1.00	16.74
3796	CB	PHE A 602	68.204	-11.538	25.161	1.00	16.06	3841	C	ASN A 608	63.201	-14.835	35.444	1.00	17.85
3797	CG	PHE A 602	68.846	-10.590	26.149	1.00	16.65	3842	O	ASN A 608	62.877	-15.128	36.608	1.00	17.58
3798	CD1	PHE A 602	68.244	-9.406	26.531	1.00	15.22	3843	CB	ASN A 608	62.493	-16.209	33.518	1.00	19.59
3799	CD2	PHE A 602	70.050	-10.983	26.751	1.00	17.45	3844	CB	ASN A 608	61.296	-16.876	32.872	1.00	22.08
3800	CE1	PHE A 602	68.808	-8.625	27.539	1.00	16.75	3845	OD1	ASN A 608	60.979	-16.711	31.678	1.00	25.08
3801	CE2	PHE A 602	70.620	-10.201	27.747	1.00	17.98	3846	ND2	ASN A 608	60.495	-17.611	33.626	1.00	20.95
3802	C7	PHE A 602	70.006	-9.011	28.135	1.00	15.11	3847	N	TYR A 609	64.415	-14.328	35.175	1.00	15.99
3803	N	VAL A 603	65.258	-11.426	26.171	1.00	15.45	3848	CA	TYR A 609	65.427	-14.137	36.228	1.00	15.94
3804	CA	VAL A 603	64.237	-10.777	27.017	1.00	15.99	3849	C	TYR A 609	64.972	-13.130	37.284	1.00	17.05
3805	C	VAL A 603	63.494	-11.778	27.884	1.00	16.06	3850	O	TYR A 609	65.128	-13.371	38.504	1.00	15.91
3806	O	VAL A 603	63.112	-11.545	29.095	1.00	16.02	3851	CB	TYR A 609	66.775	-13.708	35.575	1.00	15.56
3807	CB	VAL A 603	63.212	-9.946	26.186	1.00	18.42	3852	CG	TYR A 609	67.853	-13.313	36.573	1.00	16.22
3808	CG1	VAL A 603	62.219	-9.197	27.073	1.00	14.68	3853	CD1	TYR A 609	68.489	-14.266	37.390	1.00	16.45
3809	CG2	VAL A 603	63.961	-8.957	25.276	1.00	15.72	3854	CD2	TYR A 609	68.197	-12.002	36.736	1.00	16.36
3810	N	LEU A 604	63.039	-12.897	27.353	1.00	13.96	3855	CE1	TYR A 609	69.470	-13.877	38.289	1.00	17.53
3811	CA	LEU A 604	62.322	-13.923	28.086	1.00	15.23	3856	CE2	TYR A 609	69.169	-13.603	37.661	1.00	17.03
3812	C	LEU A 604	63.112	-14.609	29.269	1.00	17.26	3857	CZ	TYR A 609	69.731	-12.544	38.487	1.00	17.07
3813	O	LEU A 604	62.593	-14.470	30.374	1.00	14.68	3858	OH	TYR A 609	70.710	-12.140	39.389	1.00	18.77
3814	CB	LEU A 604	61.903	-15.076	27.150	1.00	18.02	3859	N	TRP A 610	64.391	-11.975	36.873	1.00	15.33
3815	CG	LEU A 604	60.794	-14.774	26.119	1.00	19.15	3860	CA	TRP A 610	63.997	-10.954	37.843	1.00	14.87
3816	CD1	LEU A 604	60.645	-15.892	25.085	1.00	19.70	3861	C	TRP A 610	62.906	-11.516	38.749	1.00	17.00
3817	CD2	LEU A 604	59.464	-14.593	26.844	1.00	21.10	3862	O	TRP A 610	62.946	-11.295	39.934	1.00	15.43
3818	N	ASP A 605	64.415	-14.727	29.072	1.00	15.26	3863	CB	TRP A 610	63.571	-9.617	37.205	1.00	16.60
3819	CA	ASP A 605	65.315	-15.216	30.095	1.00	16.47	3864	CG	TRP A 610	64.795	-8.841	36.758	1.00	17.32
3820	C	ASP A 605	65.424	-14.164	31.216	1.00	16.78	3865	CD1	TRP A 610	65.385	-8.826	35.530	1.00	18.14

3866	CD2 TRP A 610	65.604	-8.000	37.606	1.00 16.87	3911	C	HIS A 615	59.671	-10.919	43.363	1.00 18.85
3867	NE1 TRP A 610	66.501	-8.032	35.528	1.00 17.52	3912	O	HIS A 615	58.762	-10.588	44.142	1.00 19.15
3868	CE2 TRP A 610	66.670	-7.524	36.816	1.00 17.86	3913	CB	HIS A 615	60.472	-12.330	45.226	1.00 19.79
3869	CE3 TRP A 610	65.507	-7.619	38.949	1.00 16.40	3914	CG	HIS A 615	61.244	-13.480	45.789	1.00 21.80
3870	C22 TRP A 610	67.624	-6.629	37.310	1.00 17.05	3915	ND1	HIS A 615	61.349	-13.681	47.151	1.00 22.61
3871	C23 TRP A 610	66.480	-6.768	39.473	1.00 18.04	3916	CD2	HIS A 615	62.034	-14.415	45.189	1.00 23.99
3872	CH2 TRP A 610	67.519	-6.256	38.646	1.00 16.76	3917	CE1	HIS A 615	62.102	-14.765	47.345	1.00 24.07
3873	N VAL A 611	61.917	-12.259	38.217	1.00 17.68	3918	NE2	HIS A 615	62.561	-15.201	46.179	1.00 24.55
3874	CA VAL A 611	60.891	-12.872	39.051	1.00 17.19	3919	N	VAL A 616	59.898	-10.221	42.256	1.00 19.10
3875	C VAL A 611	61.481	-13.944	39.976	1.00 17.50	3920	CA	VAL A 616	59.090	-9.071	41.856	1.00 18.87
3876	O VAL A 611	61.150	-13.951	41.159	1.00 17.52	3921	C	VAL A 616	57.723	-9.605	41.412	1.00 18.87
3877	CB VAL A 611	59.784	-13.473	38.166	1.00 16.45	3922	O	VAL A 616	57.590	-10.767	41.010	1.00 16.35
3878	CG1 VAL A 611	58.825	-14.397	38.941	1.00 13.42	3923	CB	VAL A 616	59.829	-8.264	40.774	1.00 21.79
3879	CG2 VAL A 611	58.959	-12.335	37.537	1.00 15.16	3924	CG1	VAL A 616	61.242	-7.865	41.282	1.00 19.85
3880	N ASN A 612	62.221	-14.917	39.491	1.00 17.95	3925	CG2	VAL A 616	59.980	-9.080	39.511	1.00 22.01
3881	CA ASN A 612	62.770	-15.986	40.314	1.00 19.97	3926	N	ASP A 617	56.694	-8.777	41.512	1.00 16.55
3882	C ASN A 612	63.769	-15.479	41.361	1.00 20.64	3927	CA	ASP A 617	55.309	-9.174	41.337	1.00 17.29
3883	O ASN A 612	63.629	-15.773	42.566	1.00 19.49	3928	C	ASP A 617	54.694	-8.774	39.989	1.00 17.05
3884	CB ASN A 612	63.350	-17.062	39.398	1.00 23.07	3929	O	ASP A 617	53.493	-9.039	39.778	1.00 14.04
3885	CG ASN A 612	62.330	-17.925	38.661	1.00 27.67	3930	CB	ASP A 617	54.484	-8.457	42.450	1.00 15.59
3886	OD1 ASN A 612	62.706	-18.413	37.561	1.00 30.76	3931	CG	ASP A 617	55.057	-8.762	43.825	1.00 18.73
3887	ND2 ASN A 612	61.091	-18.211	39.114	1.00 23.39	3932	OD1	ASP A 617	55.655	-7.918	44.531	1.00 18.45
3888	N GLU A 613	64.794	-14.722	40.987	1.00 17.75	3933	OD2	ASP A 617	54.889	-9.919	44.243	1.00 17.15
3889	CA GLU A 613	65.784	-14.237	41.933	1.00 16.91	3934	N	GLY A 618	55.464	-8.049	39.176	1.00 15.87
3890	C GLU A 613	65.325	-13.120	42.851	1.00 16.20	3935	CA	GLY A 618	54.873	-7.628	37.888	1.00 16.30
3891	O GLU A 613	65.810	-13.011	44.017	1.00 15.78	3936	C	GLY A 618	55.813	-6.711	37.149	1.00 15.89
3892	CB GLU A 613	67.044	-13.805	41.121	1.00 17.72	3937	O	GLY A 618	56.907	-6.366	37.645	1.00 16.86
3893	CG GLU A 613	68.292	-13.483	41.942	1.00 17.78	3938	N	PHE A 619	55.484	-6.362	35.912	1.00 15.02
3894	CD GLU A 613	68.895	-14.683	42.660	1.00 19.51	3939	CA	PHE A 619	56.312	-5.472	35.083	1.00 14.50
3895	OE1 GLU A 613	68.818	-15.820	42.180	1.00 18.15	3940	C	PHE A 619	55.488	-4.376	34.420	1.00 15.17
3896	OE2 GLU A 613	69.413	-14.521	43.782	1.00 21.38	3941	O	PHE A 619	54.403	-4.681	33.856	1.00 13.52
3897	N TYR A 614	64.583	-12.123	42.358	1.00 14.53	3942	CB	PHE A 619	56.997	-6.325	33.956	1.00 14.48
3898	CA TYR A 614	64.252	-10.958	43.180	1.00 14.18	3943	CG	PHE A 619	58.073	-7.230	34.506	1.00 16.81
3899	C TYR A 614	62.805	-11.002	43.696	1.00 17.41	3944	CD1	PHE A 619	59.281	-6.690	34.973	1.00 16.56
3900	O TYR A 614	62.446	-10.102	44.461	1.00 17.30	3945	CD2	PHE A 619	57.858	-8.593	34.669	1.00 16.67
3901	CB TYR A 614	64.553	-9.677	42.390	1.00 13.30	3946	CE1	PHE A 619	60.255	-7.484	35.545	1.00 15.02
3902	CG TYR A 614	66.058	-9.370	42.201	1.00 14.37	3947	CE2	PHE A 619	58.854	-9.403	35.213	1.00 15.82
3903	CD1 TYR A 614	66.759	-8.589	43.088	1.00 14.58	3948	CZ	PHE A 619	60.044	-8.841	35.642	1.00 15.77
3904	CD2 TYR A 614	66.753	-9.907	41.128	1.00 13.92	3949	N	ARG A 620	56.013	-3.165	34.311	1.00 13.06
3905	CE1 TYR A 614	68.139	-8.317	42.936	1.00 14.22	3950	CA	ARG A 620	55.491	-2.106	33.449	1.00 14.20
3906	CE2 TYR A 614	68.120	-9.659	40.942	1.00 13.85	3951	C	ARG A 620	56.455	-1.959	32.251	1.00 13.44
3907	CZ TYR A 614	68.795	-8.864	41.857	1.00 15.00	3952	O	ARG A 620	57.627	-1.593	32.444	1.00 12.26
3908	OH TYR A 614	70.152	-8.611	41.699	1.00 13.86	3953	CB	ARG A 620	55.343	-0.758	34.177	1.00 14.29
3909	N HIS A 615	61.982	-11.968	43.309	1.00 16.00	3954	CG	ARG A 620	55.098	0.479	33.294	1.00 14.46
3910	CA HIS A 615	60.589	-12.094	43.716	1.00 18.34	3955	CD	ARG A 620	56.325	1.383	33.136	1.00 15.20

3956	NE	ARG A 620	55.937	2.660	32.513	1.00	16.32	4001	CA	LEU A 626	57.627	-2.049	20.152	1.00	17.27
3957	CZ	ARG A 620	56.625	3.360	31.605	1.00	17.13	4002	C	LEU A 626	58.090	-3.482	20.395	1.00	18.21
3958	NH1	ARG A 620	57.796	2.947	31.125	1.00	13.61	4003	O	LEU A 626	58.839	-4.029	19.551	1.00	18.64
3959	NH2	ARG A 620	56.155	4.529	31.132	1.00	15.70	4004	CB	LEU A 626	58.766	-1.121	20.566	1.00	17.52
3960	N	PHE A 621	56.083	-2.274	31.031	1.00	14.29	4005	CG	LEU A 626	58.661	0.383	20.154	1.00	17.88
3961	CA	PHE A 621	56.956	-2.250	29.884	1.00	16.71	4006	CD1	LEU A 626	59.903	1.092	20.758	1.00	16.85
3962	C	PHE A 621	56.956	-0.918	29.145	1.00	17.64	4007	CD2	LEU A 626	58.680	0.441	18.639	1.00	17.72
3963	O	PHE A 621	55.903	-0.563	28.593	1.00	16.47	4008	N	LEU A 627	57.659	-4.144	21.467	1.00	16.19
3964	CB	PHE A 621	56.636	-3.381	28.868	1.00	17.26	4009	CA	LEU A 627	58.113	-5.513	21.759	1.00	15.53
3965	CG	PHE A 621	56.868	-4.750	29.455	1.00	17.89	4010	C	LEU A 627	57.363	-6.526	20.913	1.00	16.98
3966	CD1	PHE A 621	58.079	-5.403	29.141	1.00	15.81	4011	O	LEU A 627	57.855	-7.640	20.681	1.00	17.15
3967	CD2	PHE A 621	55.812	-5.373	30.137	1.00	17.10	4012	CB	LEU A 627	57.921	-5.793	23.258	1.00	13.38
3968	CE1	PHE A 621	58.263	-6.641	29.911	1.00	16.43	4013	CG	LEU A 627	58.686	-4.849	24.212	1.00	15.02
3969	CE2	PHE A 621	56.005	-6.626	30.688	1.00	16.26	4014	CD1	LEU A 627	58.414	-5.232	25.681	1.00	15.03
3970	CZ	PHE A 621	57.224	-7.266	30.597	1.00	15.91	4015	CD2	LEU A 627	60.170	-4.930	23.934	1.00	14.76
3971	N	ASP A 622	58.055	-0.182	29.255	1.00	16.73	4016	N	GLY A 628	56.185	-6.119	20.421	1.00	17.12
3972	CA	ASP A 622	58.232	1.100	28.539	1.00	17.39	4017	CA	GLY A 628	55.382	-6.956	19.534	1.00	18.12
3973	C	ASP A 622	57.977	0.876	27.031	1.00	17.25	4018	C	GLY A 628	54.439	-7.946	20.204	1.00	17.72
3974	O	ASP A 622	58.434	-0.189	26.565	1.00	14.93	4019	O	GLY A 628	54.669	-8.439	21.306	1.00	16.57
3975	CB	ASP A 622	59.739	1.393	28.604	1.00	16.80	4020	N	LVS A 629	53.318	-8.265	19.560	1.00	18.93
3976	CG	ASP A 622	60.044	2.811	28.095	1.00	18.67	4021	CA	LVS A 629	52.277	-9.137	20.075	1.00	20.91
3977	OD1	ASP A 622	59.447	3.734	28.683	1.00	16.60	4022	C	LVS A 629	52.713	-10.539	20.453	1.00	19.69
3978	OD2	ASP A 622	60.871	2.977	27.145	1.00	18.13	4023	O	LVS A 629	52.362	-11.008	21.533	1.00	16.07
3979	N	LEU A 623	57.278	1.764	26.338	1.00	14.28	4024	CB	LVS A 629	51.156	-9.305	19.012	1.00	25.01
3980	CA	LEU A 623	56.984	1.619	24.923	1.00	15.86	4025	CG	LVS A 629	49.955	-8.430	19.255	1.00	30.66
3981	C	LEU A 623	56.733	0.197	24.536	1.00	15.06	4026	CD	LVS A 629	48.648	-9.053	18.751	1.00	34.60
3982	O	LEU A 623	57.346	-0.346	23.597	1.00	16.48	4027	CE	LVS A 629	48.662	-9.270	17.249	1.00	36.35
3983	CB	LEU A 623	58.151	2.214	24.052	1.00	14.51	4028	NZ	LVS A 629	47.246	-9.312	16.726	1.00	39.65
3984	CG	LEU A 623	58.401	3.652	24.416	1.00	16.34	4029	N	ASP A 630	53.433	-11.217	19.563	1.00	19.67
3985	CD1	LEU A 623	59.675	4.160	23.681	1.00	16.33	4030	CA	ASP A 630	53.949	-12.557	19.788	1.00	21.78
3986	CD2	LEU A 623	57.188	4.593	24.089	1.00	13.45	4031	C	ASP A 630	54.931	-12.616	20.960	1.00	19.85
3987	N	MET A 624	55.835	-0.489	25.247	1.00	15.49	4032	O	ASP A 630	54.849	-13.490	21.817	1.00	18.70
3988	CA	MET A 624	55.522	-1.877	25.003	1.00	13.19	4033	CB	ASP A 630	54.660	-13.041	18.517	1.00	26.04
3989	C	MET A 624	55.102	-2.198	23.584	1.00	16.10	4034	CG	ASP A 630	53.695	-13.269	17.360	1.00	31.74
3990	O	MET A 624	55.275	-3.346	23.112	1.00	13.77	4035	OD1	ASP A 630	54.169	-13.303	16.193	1.00	34.75
3991	CB	MET A 624	54.406	2.290	25.999	1.00	14.22	4036	OD2	ASP A 630	52.469	-13.434	17.529	1.00	33.72
3992	CG	MET A 624	54.070	-3.777	26.030	1.00	14.94	4037	N	THR A 631	55.845	-11.675	21.097	1.00	18.89
3993	SD	MET A 624	52.877	-4.324	27.305	1.00	14.57	4038	CA	THR A 631	56.697	-11.571	22.286	1.00	17.67
3994	CE	MET A 624	51.421	-3.499	26.628	1.00	14.71	4039	C	THR A 631	55.928	-11.360	23.584	1.00	17.16
3995	N	ALA A 625	54.506	-1.234	22.820	1.00	15.88	4040	O	THR A 631	56.197	-12.037	24.596	1.00	17.74
3996	CA	ALA A 625	54.068	-1.599	21.477	1.00	16.48	4041	CR	THR A 631	57.728	-10.455	22.062	1.00	16.84
3997	C	ALA A 625	55.250	2.159	20.679	1.00	16.12	4042	OG1	THR A 631	58.509	-10.815	20.895	1.00	16.86
3998	O	ALA A 625	55.086	-3.090	19.890	1.00	14.03	4043	CG2	THR A 631	58.658	-10.788	23.259	1.00	14.40
3999	CB	ALA A 625	53.509	-0.409	20.706	1.00	16.88	4044	N	MET A 632	54.947	-10.471	23.613	1.00	15.74
4000	N	LEU A 626	56.430	-1.596	20.853	1.00	16.65	4045	CA	MET A 632	54.128	10.195	24.787	1.00	16.10

4226	O	GLY A 655	58.912	8.849	19.015	1.00	24.84	4271	O	ASP A 663	50.053	-7.210	14.429	1.00	24.98
4227	N	GLY A 656	59.178	6.896	18.002	1.00	22.39	4272	CB	ASP A 663	50.219	-6.998	11.510	1.00	37.98
4228	CA	GLY A 656	59.338	7.387	16.658	1.00	24.45	4273	CG	ASP A 663	50.022	-6.418	10.118	1.00	43.25
4229	C	GLY A 656	58.840	6.337	15.661	1.00	25.22	4274	OD1	ASP A 663	51.041	-6.067	9.479	1.00	46.25
4230	O	GLY A 656	58.050	5.459	16.055	1.00	25.29	4275	OD2	ASP A 663	48.826	-6.288	9.774	1.00	46.03
4231	N	THR A 657	59.280	6.365	14.403	1.00	23.11	4276	N	GLN A 664	52.066	-6.234	14.108	1.00	22.67
4232	CA	THR A 657	58.848	5.425	13.380	1.00	23.56	4277	CA	GLN A 664	52.601	-6.838	15.333	1.00	23.37
4233	C	THR A 657	59.546	4.082	13.588	1.00	22.19	4278	C	GLN A 664	52.675	-5.789	16.432	1.00	22.24
4234	O	THR A 657	60.759	4.098	13.820	1.00	20.73	4279	O	GLN A 664	52.822	-6.210	17.585	1.00	19.91
4235	CB	THR A 657	59.256	5.972	11.983	1.00	26.11	4280	CB	GLN A 664	53.947	-7.514	15.015	1.00	23.40
4236	OG1	THR A 657	58.698	7.292	11.803	1.00	27.58	4281	CG	GLN A 664	53.799	-8.961	14.521	1.00	24.74
4237	CG2	THR A 657	58.669	5.066	10.912	1.00	26.30	4282	CD	GLN A 664	53.177	-9.871	15.593	1.00	25.49
4238	N	SER A 658	58.846	2.963	13.574	1.00	22.05	4283	OE1	GLN A 664	53.749	-9.992	16.703	1.00	24.23
4239	CA	SER A 658	59.408	1.688	13.981	1.00	22.49	4284	NE2	GLN A 664	52.036	-10.506	15.305	1.00	23.12
4240	C	SER A 658	59.740	0.805	12.779	1.00	23.91	4285	N	LEU A 665	52.600	-4.486	16.125	1.00	19.96
4241	O	SER A 658	58.952	0.966	11.879	1.00	21.76	4286	CA	LEU A 665	52.740	-3.486	17.200	1.00	19.39
4242	CB	SER A 658	58.435	0.890	14.874	1.00	20.61	4287	C	LEU A 665	51.651	-3.648	18.238	1.00	18.71
4243	OG	SER A 658	59.035	-0.398	15.133	1.00	20.61	4288	O	LEU A 665	50.488	-3.843	17.884	1.00	17.87
4244	N	GLY A 659	60.747	-0.101	12.852	1.00	22.44	4289	CB	LEU A 665	52.765	-2.046	16.656	1.00	20.03
4245	CA	GLY A 659	60.886	-1.041	11.765	1.00	22.70	4290	CG	LEU A 665	53.973	-1.662	15.786	1.00	21.89
4246	C	GLY A 659	59.939	-2.211	11.917	1.00	25.07	4291	CD1	LEU A 665	53.709	-0.411	14.951	1.00	20.88
4247	O	GLY A 659	59.836	-3.016	10.967	1.00	25.07	4292	CD2	LEU A 665	55.207	-1.501	16.668	1.00	22.05
4248	N	LEU A 660	59.245	-2.383	13.049	1.00	22.82	4293	N	VAL A 666	51.929	-3.519	19.533	1.00	18.78
4249	CA	LEU A 660	58.349	-3.534	13.163	1.00	22.64	4294	CA	VAL A 666	50.885	-3.678	20.558	1.00	18.52
4250	C	LEU A 660	57.049	-3.271	12.408	1.00	24.58	4295	C	VAL A 666	50.237	-2.321	20.883	1.00	19.69
4251	O	LEU A 660	56.462	-2.191	12.541	1.00	23.39	4296	O	VAL A 666	50.466	-1.789	21.955	1.00	17.22
4252	CB	LEU A 660	58.032	-3.798	14.656	1.00	21.87	4297	CB	VAL A 666	51.359	-4.354	21.835	1.00	16.96
4253	CG	LEU A 660	57.221	-5.073	14.921	1.00	21.46	4298	CG1	VAL A 666	50.206	-4.834	22.723	1.00	19.29
4254	CD1	LEU A 660	58.005	-6.333	14.553	1.00	21.53	4299	CG2	VAL A 666	52.295	-5.532	21.529	1.00	14.78
4255	CD2	LEU A 660	56.796	-5.118	16.387	1.00	22.01	4300	N	THR A 667	49.290	-1.919	20.033	1.00	20.48
4256	N	SER A 661	56.498	-4.299	11.768	1.00	28.28	4301	CA	THR A 667	48.502	-0.702	20.179	1.00	20.14
4257	CA	SER A 661	55.249	-4.110	11.039	1.00	31.06	4302	C	THR A 667	47.197	-1.024	20.902	1.00	18.13
4258	C	SER A 661	54.123	-3.721	11.988	1.00	31.92	4303	O	THR A 667	46.985	-2.227	21.117	1.00	16.98
4259	O	SER A 661	53.977	-4.115	13.149	1.00	30.73	4304	CB	THR A 667	48.269	-0.014	18.814	1.00	21.55
4260	CB	SER A 661	54.841	-5.369	10.278	1.00	33.28	4305	OG1	THR A 667	47.843	-1.044	17.925	1.00	20.10
4261	OG	SER A 661	54.406	-6.282	11.303	1.00	38.97	4306	CG2	THR A 667	49.597	0.611	18.281	1.00	21.18
4262	N	SER A 662	53.207	-2.944	11.425	1.00	31.42	4307	N	LYS A 668	46.331	-0.058	21.255	1.00	16.86
4263	CA	SER A 662	52.040	-2.489	12.154	1.00	31.08	4308	CA	LYS A 668	45.140	-0.468	22.022	1.00	18.52
4264	C	SER A 662	51.177	-3.592	12.719	1.00	30.70	4309	C	LYS A 668	44.229	-1.401	21.234	1.00	19.25
4265	O	SER A 662	50.577	-3.441	13.808	1.00	29.15	4310	O	LYS A 668	43.936	-1.077	20.104	1.00	15.25
4266	CB	SER A 662	51.250	-1.605	11.179	1.00	33.72	4311	CB	LYS A 668	44.277	0.724	22.546	1.00	17.82
4267	OG	SER A 662	50.239	-0.982	11.936	1.00	37.74	4312	CG	LYS A 668	45.148	1.580	23.472	1.00	19.27
4268	N	ASP A 663	51.069	-4.738	12.047	1.00	29.07	4313	CD	LYS A 668	44.324	2.507	24.357	1.00	22.35
4269	CA	ASP A 663	50.244	-5.830	12.522	1.00	30.96	4314	CE	LYS A 668	43.581	3.587	23.574	1.00	22.93
4270	C	ASP A 663	50.781	-6.442	13.814	1.00	27.66	4315	NZ	LYS A 668	44.581	4.231	22.654	1.00	24.34

43.759	-2.439	21.897	1.00	20.04	4361	C	GLY A 675	47.533	-10.238	30.385	1.00	18.93
					4362	O	GLY A 675	48.418	-10.331	31.244	1.00	17.89
					4363	N	ILE A 676	47.527	-9.199	29.566	1.00	18.34
					4364	C	ILE A 676	48.279	-7.984	29.777	1.00	18.64
45.088	-4.594	20.719	1.00	20.53	4365	C	ILE A 676	47.341	-6.773	29.627	1.00	17.75
					4366	O	ILE A 676	46.311	-6.893	28.941	1.00	16.31
					4367	CB	ILE A 676	49.479	-7.831	28.825	1.00	19.70
					4368	CG1	ILE A 676	49.028	-7.552	27.392	1.00	20.32
46.297	-6.586	21.642	1.00	20.10	4369	CG2	ILE A 676	50.426	-9.050	28.832	1.00	17.85
					4370	CD1	ILE A 676	50.167	-7.324	26.394	1.00	17.85
					4371	N	GLY A 677	47.751	-5.639	30.156	1.00	13.65
					4372	CA	GLY A 677	47.021	-4.394	30.070	1.00	15.81
44.937	-5.233	17.073	1.00	34.39	4373	C	GLY A 677	47.769	-3.254	29.403	1.00	16.01
					4374	O	GLY A 677	48.991	-3.301	29.151	1.00	16.11
					4375	N	VAL A 678	47.038	-2.172	29.079	1.00	15.57
					4376	CA	VAL A 678	47.638	-1.027	28.427	1.00	15.53
45.108	-7.890	24.371	1.00	19.04	4377	C	VAL A 678	47.199	0.251	29.119	1.00	16.70
					4378	O	VAL A 678	46.014	0.364	29.518	1.00	18.08
					4379	CB	VAL A 678	47.310	-0.949	26.919	1.00	14.79
					4380	CG1	VAL A 678	47.819	-2.120	26.065	1.00	16.01
44.177	-4.651	25.083	1.00	18.72	4381	CG2	VAL A 678	45.761	-0.920	26.704	1.00	15.88
					4382	N	PHE A 679	48.111	1.185	29.240	1.00	12.93
					4383	CA	PHE A 679	47.799	2.494	29.790	1.00	13.80
					4384	C	PHE A 679	46.705	3.036	28.866	1.00	16.99
43.957	-7.772	23.698	1.00	17.47	4385	O	PHE A 679	46.830	3.061	27.626	1.00	16.58
					4386	CB	PHE A 679	49.075	3.354	29.813	1.00	15.10
					4387	CG	PHE A 679	49.992	3.064	30.997	1.00	16.37
					4388	CD1	PHE A 679	51.234	2.485	30.823	1.00	17.10
41.622	-8.448	23.030	1.00	21.13	4389	CD2	PHE A 679	49.591	3.420	32.282	1.00	15.14
					4390	CE1	PHE A 679	52.097	2.258	31.903	1.00	17.80
					4391	CE2	PHE A 679	50.451	3.191	33.364	1.00	17.84
					4392	CZ	PHE A 679	51.687	2.594	33.195	1.00	16.20
42.644	-10.575	25.384	1.00	17.84	4393	N	ASN A 680	45.614	3.469	29.502	1.00	17.15
					4394	CA	ASN A 680	44.468	3.996	28.753	1.00	16.69
					4395	C	ASN A 680	44.612	5.491	28.529	1.00	15.66
					4396	O	ASN A 680	44.157	6.287	29.363	1.00	15.66
45.337	-11.535	26.003	1.00	16.87	4397	CB	ASN A 680	43.205	3.658	29.584	1.00	15.17
					4398	CG	ASN A 680	41.905	4.021	28.891	1.00	16.39
					4399	OD1	ASN A 680	40.786	3.672	29.326	1.00	19.69
					4400	ND2	ASN A 680	41.946	4.799	27.835	1.00	13.35
47.491	-11.905	23.957	1.00	17.85	4401	N	ASP A 681	45.204	5.905	27.392	1.00	15.34
					4402	CA	ASP A 681	45.322	7.314	27.098	1.00	17.64
					4403	C	ASP A 681	43.983	7.925	26.684	1.00	15.96
					4404	O	ASP A 681	43.930	9.146	26.750	1.00	18.29
46.351	-11.448	28.580	1.00	17.76	4405	CB	ASP A 681	46.434	7.675	26.088	1.00	16.68
					4406	CA	GLY A 675	46.690	-11.447	29.992	1.00	18.55

4406	CG	ASP	A	681	46.314	6.929	24.779	1.00	20.08	4451	O	LEU	A	687	39.835	15.949	32.801	1.00	19.35
4407	OD1	ASP	A	681	45.917	5.745	24.708	1.00	18.82	4452	CB	LEU	A	687	40.553	12.740	33.143	1.00	17.50
4408	OD2	ASP	A	681	46.590	7.570	23.728	1.00	21.03	4453	CD1	LEU	A	687	39.691	11.524	33.514	1.00	16.49
4409	N	ASN	A	682	42.939	7.183	26.388	1.00	16.19	4454	CD1	LEU	A	687	40.525	10.497	34.266	1.00	15.82
4410	CA	ASN	A	682	41.626	7.732	26.064	1.00	16.30	4455	CD2	LEU	A	687	38.459	11.960	34.349	1.00	17.74
4411	C	ASN	A	682	41.008	8.391	27.314	1.00	17.28	4456	N	ASP	A	688	41.590	15.386	31.529	1.00	19.00
4412	O	ASN	A	682	40.543	9.554	27.320	1.00	16.98	4457	CA	ASP	A	688	42.114	16.743	31.606	1.00	19.09
4413	CB	ASN	A	682	40.706	6.629	25.496	1.00	15.40	4458	C	ASP	A	688	42.632	17.315	30.289	1.00	18.61
4414	CG	ASN	A	682	41.010	6.205	24.062	1.00	17.13	4459	O	ASP	A	688	43.299	18.348	30.374	1.00	17.40
4415	OD1	ASN	A	682	41.866	6.815	23.416	1.00	16.74	4460	CB	ASP	A	688	43.247	16.843	32.624	1.00	21.76
4416	ND2	ASN	A	682	40.350	5.175	23.511	1.00	15.15	4461	CG	ASP	A	688	44.491	16.033	32.362	1.00	25.24
4417	N	ILE	A	683	41.032	7.677	28.454	1.00	16.35	4462	OD1	ASP	A	688	44.577	15.205	31.412	1.00	26.02
4418	CA	ILE	A	683	40.470	8.220	29.694	1.00	16.07	4463	OD2	ASP	A	688	45.452	16.200	33.160	1.00	24.89
4419	C	ILE	A	683	41.284	9.380	30.251	1.00	17.30	4464	N	GLY	A	689	42.237	16.788	29.143	1.00	19.33
4420	O	ILE	A	683	40.836	10.455	30.737	1.00	17.55	4465	CA	GLY	A	689	42.679	17.411	27.872	1.00	20.12
4421	CB	ILE	A	683	40.228	7.122	30.748	1.00	16.73	4466	C	GLY	A	689	43.852	16.650	27.244	1.00	21.08
4422	CG1	ILE	A	683	39.118	7.666	31.683	1.00	17.76	4467	O	GLY	A	689	44.631	15.975	27.940	1.00	18.25
4423	CG2	ILE	A	683	41.474	6.693	31.535	1.00	13.77	4468	N	ASN	A	690	43.957	16.778	25.912	1.00	20.39
4424	CD1	ILE	A	683	38.930	6.930	32.986	1.00	18.13	4469	CA	ASN	A	690	45.008	16.103	25.159	1.00	18.52
4425	N	ARG	A	684	42.600	9.261	30.064	1.00	15.73	4470	C	ASN	A	690	46.382	16.400	25.702	1.00	18.62
4426	CA	ARG	A	684	43.514	10.306	30.488	1.00	16.66	4471	O	ASN	A	690	46.767	17.560	25.942	1.00	18.86
4427	C	ARG	A	684	43.207	11.587	29.736	1.00	15.87	4472	CB	ASN	A	690	44.883	16.503	23.659	1.00	20.87
4428	O	ARG	A	684	43.115	12.677	30.317	1.00	16.71	4473	CG	ASN	A	690	45.899	15.668	22.877	1.00	22.43
4429	CB	ARG	A	684	44.976	9.857	30.262	1.00	18.05	4474	OD1	ASN	A	690	47.036	16.114	22.664	1.00	22.38
4430	CG	ARG	A	684	45.952	10.905	30.788	1.00	20.35	4475	ND2	ASN	A	690	45.472	14.460	22.513	1.00	21.21
4431	CD	ARG	A	684	47.222	11.054	30.003	1.00	26.33	4476	N	VAL	A	691	47.256	15.408	25.828	1.00	17.79
4432	NE	ARG	A	684	47.113	11.061	28.560	1.00	30.02	4477	CA	VAL	A	691	48.582	15.528	26.410	1.00	20.26
4433	CZ	ARG	A	684	48.001	10.589	27.682	1.00	32.36	4478	C	VAL	A	691	49.536	16.419	25.616	1.00	20.63
4434	NH1	ARG	A	684	49.205	10.033	27.964	1.00	33.59	4479	O	VAL	A	691	50.503	16.940	26.182	1.00	19.98
4435	NH2	ARG	A	684	47.644	10.673	26.404	1.00	33.28	4480	CB	VAL	A	691	49.204	14.114	26.594	1.00	21.95
4436	N	ASN	A	685	43.193	11.515	28.410	1.00	15.54	4481	CG1	VAL	A	691	49.485	13.451	25.233	1.00	19.94
4437	CA	ASN	A	685	42.944	12.721	27.596	1.00	17.75	4482	CG2	VAL	A	691	50.487	14.150	27.404	1.00	21.70
4438	C	ASN	A	685	41.554	13.294	27.914	1.00	16.60	4483	N	PHE	A	692	49.287	16.668	24.331	1.00	19.63
4439	O	ASN	A	685	41.377	14.510	27.960	1.00	16.32	4484	CA	PHE	A	692	50.187	17.533	23.544	1.00	20.10
4440	CB	ASN	A	685	43.101	12.404	26.078	1.00	15.79	4485	C	PHE	A	692	49.799	19.008	23.561	1.00	18.56
4441	CG	ASN	A	685	44.559	12.204	25.670	1.00	17.29	4486	O	PHE	A	692	50.399	19.821	22.869	1.00	18.61
4442	OD1	ASN	A	685	45.564	12.731	26.189	1.00	15.27	4487	CB	PHE	A	692	50.238	17.053	22.090	1.00	18.53
4443	ND2	ASN	A	685	44.757	11.357	24.661	1.00	18.75	4488	CG	PHE	A	692	50.859	15.694	21.969	1.00	21.54
4444	N	GLY	A	686	40.581	12.454	28.172	1.00	16.82	4489	CD1	PHE	A	692	50.085	14.538	21.907	1.00	20.75
4445	CA	GLY	A	686	39.208	12.841	28.482	1.00	18.79	4490	CD2	PHE	A	692	52.245	15.579	21.964	1.00	21.43
4446	C	GLY	A	686	39.085	13.538	29.825	1.00	18.90	4491	CE1	PHE	A	692	50.723	13.309	21.812	1.00	21.57
4447	O	GLY	A	686	38.321	14.506	29.982	1.00	18.03	4492	CE2	PHE	A	692	52.865	14.348	21.891	1.00	21.34
4448	N	LEU	A	687	39.870	13.071	30.804	1.00	18.75	4493	CZ	PHE	A	692	52.097	13.205	21.793	1.00	21.14
4449	CA	LEU	A	687	39.858	13.683	32.131	1.00	17.87	4494	N	ASP	A	693	48.780	19.382	24.314	1.00	19.75
4450	C	LEU	A	687	40.445	15.084	32.155	1.00	19.56	4495	CA	ASP	A	693	48.307	20.760	24.442	1.00	18.18

896	N	THR A 232	33.400	-10.266	-19.692	1.00	30.00	941	OE1	GLU A 238	36.045	-17.645	-17.053	1.00	39.51
897	CA	THR A 232	32.070	-10.894	-19.612	1.00	32.54	942	OE2	GLU A 238	34.397	-18.708	-17.948	1.00	39.63
898	C	THR A 232	32.246	-12.342	-19.188	1.00	32.86	943	N	LYS A 239	35.917	-19.366	-12.434	1.00	31.34
899	O	THR A 232	33.069	-13.072	-19.750	1.00	32.67	944	CA	LYS A 239	36.752	-18.708	-12.071	1.00	30.50
900	CB	THR A 232	31.143	-10.753	-20.806	1.00	33.54	945	C	LYS A 239	38.005	-18.078	-12.734	1.00	29.49
901	OG1	THR A 232	31.043	-11.964	-21.567	1.00	37.56	946	O	LYS A 239	38.644	-18.729	-13.541	1.00	26.10
902	CG2	THR A 232	31.478	-9.607	-21.734	1.00	30.68	947	CB	LYS A 239	37.649	-19.635	-11.230	1.00	30.57
903	N	VAL A 233	31.540	-12.713	-18.135	1.00	33.79	948	CB	LYS A 239	39.081	-19.338	-10.780	1.00	32.75
904	CA	VAL A 233	31.579	-14.068	-17.613	1.00	36.22	949	CD	LYS A 239	39.203	-19.871	-9.351	1.00	35.35
905	C	VAL A 233	30.298	-14.809	-17.947	1.00	38.71	950	CD	LYS A 239	39.279	-21.314	-8.840	1.00	36.50
906	O	VAL A 233	29.186	-14.331	-17.740	1.00	37.77	951	NZ	LYS A 239	39.762	-21.354	-7.461	1.00	33.54
907	CB	VAL A 233	31.792	-13.955	-16.105	1.00	35.04	952	N	VAL A 240	38.248	-16.787	-12.495	1.00	26.95
908	CG1	VAL A 233	31.838	-15.338	-15.489	1.00	35.88	953	CA	VAL A 240	39.095	-15.992	-13.399	1.00	23.70
909	CG2	VAL A 233	33.107	-13.252	-15.847	1.00	33.72	954	C	VAL A 240	40.437	-15.350	-11.538	1.00	23.90
910	N	PRO A 234	30.486	-16.031	-18.513	1.00	41.11	955	O	VAL A 240	40.419	-15.640	-12.743	1.00	25.44
911	CA	PRO A 234	29.393	-16.841	-19.027	1.00	42.50	956	CB	VAL A 240	38.369	-14.708	-13.849	1.00	22.65
912	C	PRO A 234	28.491	-17.443	-17.947	1.00	43.33	957	CG1	VAL A 240	39.170	-13.901	-14.866	1.00	22.07
913	O	PRO A 234	28.940	-17.865	-16.889	1.00	45.44	958	CG2	VAL A 240	36.957	-14.947	-14.404	1.00	21.34
914	CB	PRO A 234	29.993	-18.031	-19.783	1.00	41.71	959	N	THR A 241	41.505	-15.654	-13.524	1.00	24.76
915	CG	PRO A 234	31.509	-17.862	-19.793	1.00	42.81	960	CA	THR A 241	42.835	-15.308	-13.067	1.00	26.11
916	CD	PRO A 234	31.725	-16.769	-18.640	1.00	40.20	961	C	THR A 241	43.244	-13.957	-13.689	1.00	26.23
917	N	GLN A 235	27.199	-17.504	-18.314	1.00	20.00	962	O	THR A 241	43.165	-13.786	-14.922	1.00	24.94
918	CA	GLN A 235	26.246	-18.000	-17.341	1.00	20.00	963	CB	THR A 241	43.856	-16.397	-13.451	1.00	26.92
919	C	GLN A 235	26.543	-19.290	-16.567	1.00	20.00	964	CG1	THR A 241	43.594	-17.610	-12.693	1.00	29.26
920	O	GLN A 235	26.691	-20.364	-17.135	1.00	20.00	965	N	PHE A 242	45.285	-15.969	-13.169	1.00	25.11
921	CB	GLN A 235	24.891	-18.189	-18.091	0.00	20.00	966	N	PHE A 242	43.659	-13.013	-12.870	1.00	23.69
922	CG	GLN A 235	23.744	-18.642	-17.182	0.00	20.00	967	CA	PHE A 242	44.060	-11.655	-13.229	1.00	22.06
923	CD	GLN A 235	22.488	-18.822	-18.002	0.00	20.00	968	C	PHE A 242	45.557	-11.465	-12.984	1.00	22.71
924	OE1	GLN A 235	21.427	-19.185	-17.522	0.00	20.00	969	O	PHE A 242	46.093	-11.901	-11.969	1.00	22.30
925	NE2	GLN A 235	22.653	-18.554	-19.313	0.00	20.00	970	CB	PHE A 242	43.275	-10.648	-12.369	1.00	22.34
926	N	GLY A 236	26.571	-19.113	-15.235	1.00	20.00	971	CG	PHE A 242	41.777	-10.695	-12.505	1.00	22.23
927	CA	GLY A 236	26.914	-20.255	-14.411	1.00	20.00	972	CD1	PHE A 242	41.137	-9.866	-13.423	1.00	21.94
928	C	GLY A 236	28.215	-19.843	-13.723	1.00	20.00	973	CD2	PHE A 242	40.996	-11.545	-11.747	1.00	21.82
929	O	GLY A 236	28.571	-20.322	-12.660	1.00	20.00	974	CE1	PHE A 242	39.763	-9.870	-13.559	1.00	21.82
930	N	GLY A 237	28.951	-18.960	-14.432	1.00	45.11	975	CE2	PHE A 242	39.622	-11.580	-11.923	1.00	21.18
931	CA	GLY A 237	30.099	-18.275	-13.853	1.00	43.81	976	CZ	PHE A 242	38.986	-10.744	-12.823	1.00	21.58
932	C	GLY A 237	31.386	-19.060	-14.065	1.00	41.23	977	N	THR A 243	46.285	-10.845	-13.922	1.00	20.68
933	O	GLY A 237	31.412	-20.077	-14.716	1.00	41.47	978	CA	THR A 243	47.718	-10.737	-13.888	1.00	21.11
934	N	GLU A 238	32.494	-18.495	-13.570	1.00	39.53	979	C	THR A 243	48.264	-9.334	-14.094	1.00	21.20
935	CA	GLU A 238	33.738	-19.269	-13.544	1.00	36.93	980	O	THR A 243	47.787	-8.652	-14.989	1.00	19.64
936	C	GLU A 238	34.814	-18.623	-12.658	1.00	35.69	981	CB	THR A 243	48.327	-11.664	-14.974	1.00	22.96
937	O	GLU A 238	34.687	-17.510	-12.178	1.00	34.73	982	OG1	THR A 243	47.919	-13.047	-14.785	1.00	24.34
938	CB	GLU A 238	34.249	-19.376	-14.974	1.00	37.46	983	CG2	THR A 243	49.846	-11.654	-14.938	1.00	23.70
939	CG	GLU A 238	34.152	-18.042	-15.715	1.00	38.60	984	N	TYR A 244	49.357	-8.991	-13.418	1.00	21.69
940	CD	GLU A 238	34.928	-18.141	-17.002	1.00	38.06	985	CA	TYR A 244	50.053	-7.712	-13.568	1.00	22.20

986	C	TYR A 244	51.558	-7.971	-13.653	1.00	22.75	1031	ND2 ASN A 249	54.530	0.640	-16.173	1.00	24.05
987	O	TYR A 244	52.094	-8.753	-12.862	1.00	23.82	1032	N GLN A 250	51.086	-4.178	-17.796	1.00	22.09
988	CB	TYR A 244	49.763	-6.781	-12.377	1.00	22.63	1033	CA GLN A 250	50.791	-4.759	-18.599	1.00	21.69
989	CG	TYR A 244	50.523	-5.466	-12.369	1.00	22.04	1034	C GLN A 250	49.029	-5.589	-17.734	1.00	22.85
990	CD1	TYR A 244	50.308	-4.453	-13.300	1.00	20.84	1035	O GLN A 250	50.263	-6.152	-16.701	1.00	20.61
991	CD2	TYR A 244	51.477	-5.248	-11.386	1.00	22.48	1036	CB GLN A 250	51.375	-5.611	-19.720	1.00	22.60
992	CE1	TYR A 244	51.053	-3.287	-13.268	1.00	21.71	1037	CG GLN A 250	52.265	-4.859	-20.720	1.00	23.80
993	CE2	TYR A 244	52.175	-4.046	-11.292	1.00	22.10	1038	CD GLN A 250	51.509	-3.725	-21.387	1.00	25.16
994	CZ	TYR A 244	51.961	-3.071	-12.249	1.00	21.72	1039	OE1 GLN A 250	50.566	-3.959	-22.167	1.00	24.30
995	OH	TYR A 244	52.682	-1.888	-12.195	1.00	21.67	1040	NE2 GLN A 250	51.806	-2.490	-20.991	1.00	25.44
996	N	ILE A 245	52.258	-7.381	-14.614	1.00	21.91	1041	N VAL A 251	48.526	-5.568	-18.077	1.00	21.86
997	CA	ILE A 245	53.672	-7.500	-14.845	1.00	21.21	1042	CA VAL A 251	47.558	-6.304	-17.262	1.00	21.68
998	C	ILE A 245	54.326	-6.151	-14.564	1.00	22.31	1043	C VAL A 251	46.690	-7.203	-18.149	1.00	21.54
999	O	ILE A 245	54.133	-5.163	-15.266	1.00	20.02	1044	O VAL A 251	46.351	-6.836	-19.273	1.00	19.04
1000	CB	ILE A 245	53.947	-7.953	-16.298	1.00	22.59	1045	CB VAL A 251	46.680	-5.498	-16.291	1.00	23.56
1001	CG1	ILE A 245	53.225	-9.298	-16.560	1.00	23.96	1046	CG1 VAL A 251	47.093	-4.039	-16.093	1.00	22.08
1002	CG2	ILE A 245	55.434	-8.035	-16.554	1.00	18.24	1047	CG2 VAL A 251	45.175	-5.587	-16.451	1.00	22.66
1003	CD1	ILE A 245	53.736	-10.007	-17.795	1.00	27.43	1048	N PHE A 252	46.486	-8.436	-17.687	1.00	20.51
1004	N	PRO A 246	54.950	-6.024	-13.382	1.00	23.34	1049	CA PHE A 252	45.764	-9.449	-18.458	1.00	21.29
1005	CA	PRO A 246	55.533	-4.759	-12.930	1.00	23.67	1050	C PHE A 252	44.747	-10.183	-17.592	1.00	22.46
1006	C	PRO A 246	56.506	-4.124	-13.911	1.00	22.46	1051	O PHE A 252	44.936	-10.267	-16.368	1.00	24.63
1007	O	PRO A 246	56.416	-2.914	-14.115	1.00	22.69	1052	CB PHE A 252	46.763	-10.520	-18.984	1.00	18.87
1008	CB	PRO A 246	56.242	-5.151	-11.622	1.00	23.64	1053	CG PHE A 252	47.927	-9.918	-19.740	1.00	19.77
1009	CG	PRO A 246	55.416	-6.302	-11.119	1.00	22.55	1054	CD1 PHE A 252	47.771	-9.602	-21.089	1.00	19.15
1010	CD	PRO A 246	55.177	-7.102	-12.400	1.00	23.30	1055	CD2 PHE A 252	49.087	-9.536	-19.076	1.00	19.82
1011	N	SER A 247	57.418	-4.864	-14.543	1.00	21.20	1056	CE1 PHE A 252	48.807	-9.007	-21.784	1.00	18.25
1012	CA	SER A 247	58.360	-4.243	-15.475	1.00	23.73	1057	CE2 PHE A 252	50.125	-8.926	-19.777	1.00	21.04
1013	C	SER A 247	57.762	-3.511	-16.663	1.00	24.65	1058	CZ PHE A 252	49.981	-8.666	-21.127	1.00	19.76
1014	O	SER A 247	58.401	-2.582	-17.178	1.00	24.40	1059	N ASP A 253	43.766	-10.823	-18.207	1.00	21.21
1015	CB	SER A 247	59.408	-5.238	-16.041	1.00	23.42	1060	CA ASP A 253	42.883	-11.739	-17.490	1.00	21.71
1016	OG	SER A 247	58.758	-6.211	-16.858	1.00	23.25	1061	C ASP A 253	42.766	-13.015	-18.357	1.00	23.08
1017	N	THR A 248	56.656	-3.993	-17.221	1.00	23.91	1062	O ASP A 253	42.922	-12.971	-19.582	1.00	20.43
1018	CA	THR A 248	56.010	-3.307	-18.332	1.00	23.41	1063	CB ASP A 253	41.525	-11.192	-17.091	1.00	23.51
1019	C	THR A 248	54.687	-2.652	-17.942	1.00	23.60	1064	CG ASP A 253	40.668	-10.833	-18.296	1.00	23.59
1020	O	THR A 248	54.054	-1.971	-18.736	1.00	21.55	1065	OD1 ASP A 253	40.153	-11.833	-18.864	1.00	23.59
1021	CB	THR A 248	55.680	-4.349	-19.443	1.00	22.17	1066	OD2 ASP A 253	40.550	-9.643	-18.650	1.00	22.42
1022	OG1	THR A 248	54.807	-5.326	-18.855	1.00	17.24	1067	N SER A 254	42.493	-14.153	-17.717	1.00	21.89
1023	CG2	THR A 248	56.993	-5.005	-19.903	1.00	21.11	1068	CA SER A 254	42.414	-15.435	-18.370	1.00	23.57
1024	N	ASN A 249	54.184	-2.889	-16.740	1.00	22.61	1069	C SER A 254	41.210	-15.586	-19.294	1.00	25.86
1025	CA	ASN A 249	52.883	-2.425	-16.291	1.00	22.91	1070	O SER A 254	41.180	-16.566	-20.049	1.00	25.58
1026	C	ASN A 249	51.737	-3.081	-17.080	1.00	20.56	1071	CB SER A 254	42.435	-16.597	-17.360	1.00	23.34
1027	O	ASN A 249	50.625	-2.569	-16.955	1.00	20.56	1072	OG SER A 254	41.247	-16.555	-16.579	1.00	24.91
1028	CB	ASN A 249	52.698	-0.900	-16.304	1.00	22.75	1073	N VAL A 255	40.213	-14.721	-19.243	1.00	26.09
1029	CG	ASN A 249	53.754	-0.182	-15.455	1.00	25.70	1074	CA VAL A 255	39.076	-14.799	-20.148	1.00	28.53
1030	OD1	ASN A 249	53.878	-0.393	-14.245	1.00	24.53	1075	C VAL A 255	39.390	-14.071	-21.453	1.00	27.79

1166	C	ALA A 267	64.766	-7.194	-17.577	1.00	40.22	1211	CD2 LEU A 273	65.279	-2.514	-1.136	1.00	25.15
1167	O	ALA A 267	63.560	-7.315	-17.771	1.00	38.69	1212	N VAL A 274	68.455	-4.706	-4.675	1.00	24.94
1168	CB	ALA A 267	66.132	-9.162	-18.339	1.00	39.06	1213	CA VAL A 274	68.417	-5.999	-5.341	1.00	26.05
1169	N	GLY A 268	65.403	-6.030	-17.573	1.00	42.28	1214	C VAL A 274	68.515	-7.184	-4.379	1.00	26.04
1170	CA	GLY A 268	64.752	-4.784	-17.865	1.00	44.37	1215	O VAL A 274	69.229	-7.097	-3.381	1.00	26.70
1171	C	GLY A 268	64.348	-3.978	-16.643	1.00	46.77	1216	CB VAL A 274	69.583	-6.171	-6.361	1.00	25.86
1172	O	GLY A 268	64.299	-2.737	-16.795	1.00	47.62	1217	CG1 VAL A 274	69.620	-5.082	-7.432	1.00	25.76
1173	N	VAL A 269	64.052	-4.595	-15.480	1.00	46.24	1218	CG2 VAL A 274	70.921	-6.116	-5.640	1.00	26.10
1174	CA	VAL A 269	63.594	-3.736	-14.385	1.00	45.82	1219	N GLN A 275	67.836	-8.261	-4.692	1.00	25.69
1175	C	VAL A 269	64.666	-2.835	-13.801	1.00	44.79	1220	CA GLN A 275	67.948	-9.534	-4.016	1.00	27.38
1176	O	VAL A 269	65.871	-3.071	-13.802	1.00	44.61	1221	C GLN A 275	68.722	-10.509	-4.924	1.00	26.18
1177	CB	VAL A 269	62.762	-4.389	-13.300	1.00	47.26	1222	O GLN A 275	68.335	-10.671	-6.064	1.00	24.99
1178	CG1	VAL A 269	61.276	-4.187	-13.663	1.00	47.77	1223	CB GLN A 275	66.596	-10.143	-3.662	1.00	26.97
1179	CG2	VAL A 269	62.947	-5.864	-13.074	1.00	47.82	1224	CG GLN A 275	66.671	-11.477	-2.930	1.00	28.59
1180	N	GLN A 270	64.168	-1.666	-13.364	1.00	44.38	1225	CD GLN A 275	65.265	-11.964	-2.607	1.00	32.32
1181	CA	GLN A 270	65.117	-0.651	-12.866	1.00	43.41	1226	OE1 GLN A 275	64.501	-11.303	-1.895	1.00	33.16
1182	C	GLN A 270	65.016	-0.541	-11.348	1.00	39.99	1227	NE2 GLN A 275	64.893	-13.118	-3.136	1.00	32.96
1183	O	GLN A 270	63.909	-0.536	-10.823	1.00	39.03	1228	N LEU A 276	69.837	-11.012	-4.427	1.00	25.42
1184	CB	GLN A 270	64.909	0.628	-13.663	1.00	44.70	1229	CA LEU A 276	70.597	-11.944	-5.130	1.00	25.50
1185	CG	GLN A 270	63.545	1.259	-13.564	1.00	46.40	1230	C LEU A 276	70.562	-13.358	-4.573	1.00	26.02
1186	CD	GLN A 270	63.594	2.718	-14.049	1.00	48.21	1231	O LEU A 276	70.448	-13.492	-3.342	1.00	26.72
1187	OE1	GLN A 270	63.352	3.648	-13.263	1.00	49.65	1232	CB LEU A 276	72.157	-11.498	-5.051	1.00	23.09
1188	NE2	GLN A 270	63.949	2.916	-15.320	1.00	47.11	1233	CG LEU A 276	72.473	-10.046	-5.406	1.00	24.38
1189	N	THR A 271	66.168	-0.620	-10.661	1.00	36.93	1234	CD1 LEU A 276	73.930	-9.640	-5.129	1.00	23.10
1190	CA	THR A 271	66.136	-0.641	-9.198	1.00	32.17	1235	CD2 LEU A 276	72.373	-9.799	-6.886	1.00	22.76
1191	C	THR A 271	67.457	-0.271	-8.565	1.00	31.16	1236	N THR A 277	70.615	-14.370	-5.434	1.00	24.89
1192	O	THR A 271	68.558	-0.403	-9.078	1.00	29.69	1237	CA THR A 277	70.574	-15.758	-5.009	1.00	24.89
1193	CB	THR A 271	65.681	-2.033	-8.683	1.00	32.24	1238	C THR A 277	71.967	-16.301	-5.329	1.00	25.72
1194	OG1	THR A 271	65.608	-2.075	-7.243	1.00	30.97	1239	O THR A 277	72.476	-15.942	-6.401	1.00	26.30
1195	CG2	THR A 271	66.584	-3.179	-9.133	1.00	30.31	1240	CB THR A 277	69.479	-16.586	-5.694	1.00	27.01
1196	N	ASN A 272	67.330	0.245	-7.332	1.00	28.98	1241	OG1 THR A 277	68.199	-15.975	-5.436	1.00	27.31
1197	CA	ASN A 272	68.481	0.558	-6.529	1.00	26.71	1242	CG2 THR A 277	69.423	-18.028	-5.179	1.00	25.75
1198	C	ASN A 272	68.527	-0.399	-5.322	1.00	24.87	1243	N LEU A 278	72.567	-17.086	-4.445	1.00	24.33
1199	O	ASN A 272	69.417	-0.272	-4.515	1.00	22.11	1244	CA LEU A 278	73.924	-17.581	-4.635	1.00	25.40
1200	CB	ASN A 272	68.464	2.031	-6.162	1.00	27.42	1245	C LEU A 278	72.925	-19.707	-4.513	1.00	25.92
1201	CG	ASN A 272	67.423	2.457	-5.152	1.00	27.32	1246	O LEU A 278	74.755	-17.375	-3.349	1.00	24.44
1202	OD1	ASN A 272	67.473	3.640	-4.735	1.00	28.32	1247	CB LEU A 278	74.785	-15.959	-2.779	1.00	25.93
1203	ND2	ASN A 272	66.516	1.631	-4.751	1.00	25.56	1248	CG LEU A 278	75.228	-14.960	-3.842	1.00	25.13
1204	N	LEU A 273	67.770	-1.488	-5.320	1.00	24.32	1249	CD1 LEU A 278	75.676	-15.830	-1.528	1.00	25.09
1205	CA	LEU A 273	67.740	-2.431	-4.206	1.00	24.89	1250	CD2 LEU A 278	74.866	-19.602	-5.666	1.00	25.25
1206	C	LEU A 273	67.477	-3.819	-4.758	1.00	24.94	1251	N ALA A 279	74.847	-21.038	-5.956	1.00	27.68
1207	O	LEU A 273	66.401	-4.035	-5.326	1.00	23.57	1252	CA ALA A 279	75.156	-21.861	-4.701	1.00	26.75
1208	CB	LEU A 273	66.640	-2.010	-3.197	1.00	25.97	1253	C ALA A 279	74.770	-23.030	-4.671	1.00	25.73
1209	CG	LEU A 273	66.566	-2.816	-1.893	1.00	24.77	1254	O ALA A 279	75.804	-21.373	-7.095	1.00	27.60
1210	CD1	LEU A 273	67.763	-2.539	-0.981	1.00	23.86	1255	CB ALA A 279					

1436	NH2	ARG	A	303	67.226	-6.920	5.887	1.00	17.39	1491	CG	PRO	A	309	65.446	-23.573	11.949	1.00	19.19
1437	N	ASN	A	304	69.665	-11.600	8.626	1.00	14.70	1492	CD	PRO	A	309	66.282	-22.609	11.100	1.00	19.26
1438	CA	ASN	A	304	68.496	-12.476	8.741	1.00	14.47	1493	CA	ARG	A	310	69.744	-23.653	12.564	1.00	18.57
1439	C	ASN	A	304	68.829	-13.961	8.551	1.00	15.73	1494	N	ARG	A	310	71.114	-24.027	12.882	1.00	18.99
1440	O	ASN	A	304	68.090	-14.850	8.955	1.00	16.46	1495	C	ARG	A	310	71.813	-23.033	13.806	1.00	20.10
1441	CB	ASN	A	304	67.423	-12.026	7.748	1.00	14.98	1496	O	ARG	A	310	72.758	-23.400	14.544	1.00	19.39
1442	CG	ASN	A	304	66.623	-10.906	8.362	1.00	15.04	1497	CB	ARG	A	310	71.910	-24.244	11.582	1.00	21.29
1443	OD1	ASN	A	304	66.852	-10.495	9.494	1.00	16.92	1498	CG	ARG	A	310	72.315	-22.947	10.876	1.00	23.49
1444	ND2	ASN	A	304	65.660	-10.396	7.575	1.00	14.95	1499	CD	ARG	A	310	73.173	-23.235	9.648	1.00	25.45
1445	N	VAL	A	305	69.997	-14.272	8.008	1.00	15.65	1499	NE	ARG	A	310	74.564	-23.436	10.024	1.00	30.55
1446	CA	VAL	A	305	70.457	-15.659	7.877	1.00	15.60	1491	CZ	ARG	A	310	75.583	-23.674	9.187	1.00	33.31
1447	C	VAL	A	305	70.641	-16.261	9.281	1.00	14.99	1492	NH1	ARG	A	310	75.463	-23.744	7.854	1.00	33.05
1448	O	VAL	A	305	70.346	-17.453	9.542	1.00	13.78	1493	NH2	ARG	A	310	76.793	-23.814	9.703	1.00	33.33
1449	CB	VAL	A	305	71.763	-15.754	7.057	1.00	16.12	1494	N	TVR	A	311	71.378	-21.761	13.838	1.00	18.74
1450	CG1	VAL	A	305	72.886	-15.007	7.820	1.00	16.01	1495	CA	TVR	A	311	71.933	-20.818	14.800	1.00	19.14
1451	CG2	VAL	A	305	72.211	-17.204	6.923	1.00	14.70	1496	C	TVR	A	311	71.067	-20.575	16.024	1.00	19.76
1452	N	LEU	A	306	70.943	-15.455	10.302	1.00	15.35	1497	O	TVR	A	311	71.260	-19.550	16.682	1.00	19.20
1453	CA	LEU	A	306	71.061	-15.925	11.682	1.00	16.85	1498	CB	TVR	A	311	72.119	-19.454	14.074	1.00	20.52
1454	C	LEU	A	306	69.742	-16.291	12.359	1.00	16.79	1499	CG	TVR	A	311	72.341	-19.445	11.558	1.00	20.06
1455	O	LEU	A	306	69.821	-16.866	13.444	1.00	16.11	1500	CD1	TVR	A	311	74.254	-20.025	12.854	1.00	19.22
1456	CB	LEU	A	306	71.854	-14.947	12.574	1.00	17.30	1501	CD2	TVR	A	311	73.093	-19.612	10.395	1.00	21.56
1457	CG	LEU	A	306	73.183	-14.497	11.943	1.00	18.98	1502	CE1	TVR	A	311	75.018	-20.203	11.703	1.00	20.95
1458	CD1	LEU	A	306	73.755	-13.292	12.719	1.00	21.71	1503	CE2	TVR	A	311	74.425	-19.993	10.480	1.00	21.56
1459	CD2	LEU	A	306	74.171	-15.623	11.853	1.00	17.50	1504	CZ	TVR	A	311	75.159	-20.170	9.329	1.00	24.43
1460	N	ASN	A	307	68.579	-16.074	11.742	1.00	17.17	1505	OH	TVR	A	311	70.069	-21.385	16.314	1.00	22.16
1461	CA	ASN	A	307	67.295	-16.537	12.219	1.00	19.40	1506	N	ASP	A	312	69.147	-21.132	17.421	1.00	24.33
1462	C	ASN	A	307	67.118	-18.065	11.996	1.00	22.23	1507	CA	ASP	A	312	69.426	-21.956	18.667	1.00	22.29
1463	O	ASN	A	307	66.235	-18.629	12.645	1.00	19.61	1508	C	ASP	A	312	69.166	-23.155	18.676	1.00	22.82
1464	CB	ASN	A	307	66.072	-15.914	11.520	1.00	17.50	1509	O	ASP	A	312	67.703	-21.360	16.940	1.00	25.85
1465	CG	ASN	A	307	65.952	-14.411	11.499	1.00	19.19	1510	CB	ASP	A	312	66.717	-20.989	18.046	1.00	30.43
1466	OD1	ASN	A	307	66.604	-13.703	12.268	1.00	16.40	1511	CG	ASP	A	312	66.756	-19.889	18.609	1.00	30.37
1467	ND2	ASN	A	307	65.093	-13.861	10.615	1.00	16.76	1512	OD1	ASP	A	312	65.841	-21.814	18.382	1.00	33.45
1468	N	LEU	A	308	67.846	-18.698	11.079	1.00	20.99	1513	OD2	ASP	A	312	69.905	-21.325	19.725	1.00	21.56
1469	CA	LEU	A	308	67.709	-20.121	10.793	1.00	20.83	1514	N	TVR	A	313	70.305	-22.052	20.933	1.00	21.31
1470	C	LEU	A	308	67.998	-21.006	11.995	1.00	21.03	1515	CA	TVR	A	313	69.224	-21.924	21.996	1.00	22.83
1471	O	LEU	A	308	68.784	-20.723	12.906	1.00	18.48	1516	C	TVR	A	313	58.987	-20.799	22.457	1.00	20.91
1472	CB	LEU	A	308	68.641	-20.561	9.636	1.00	21.47	1517	O	TVR	A	313	71.644	-21.503	21.452	1.00	20.67
1473	CG	LEU	A	308	68.405	-19.861	8.291	1.00	23.03	1518	CB	TVR	A	313	72.137	-22.255	22.674	1.00	19.10
1474	CD1	LEU	A	308	69.489	-20.134	7.261	1.00	23.09	1519	CG	TVR	A	313	72.697	-23.521	22.532	1.00	18.67
1475	CD2	LEU	A	308	67.039	-20.248	7.739	1.00	21.71	1520	CD1	TVR	A	313	71.998	-21.744	23.956	1.00	18.42
1476	N	PRO	A	309	67.320	-22.166	12.049	1.00	20.22	1521	CD2	TVR	A	313	73.148	-24.247	23.621	1.00	19.13
1477	CA	PRO	A	309	67.416	-23.095	13.161	1.00	19.80	1522	CE1	TVR	A	313	72.416	-22.475	25.069	1.00	17.61
1478	C	PRO	A	309	68.812	-23.561	13.507	1.00	19.00	1523	CE2	TVR	A	313	72.994	-23.703	24.889	1.00	19.22
1479	O	PRO	A	309	69.113	-23.663	14.715	1.00	19.17	1524	CZ	TVR	A	313	73.413	-24.442	25.989	1.00	18.27
1480	CB	PRO	A	309	66.476	-24.256	12.793	1.00	20.37	1525	OH	TVR	A	313					

1526	N	SER A 314	68.599	-23.055	22.329	1.00	23.06	1571	ND2 ASN A 320	78.589	-14.900	35.304	1.00	18.55
1527	CA	SER A 314	67.542	-23.000	23.332	1.00	25.19	1572	N VAL A 321	77.797	-19.940	35.176	1.00	22.76
1528	C	SER A 314	67.926	-23.474	24.719	1.00	25.25	1573	CA VAL A 321	77.084	-20.812	36.124	1.00	22.43
1529	O	SER A 314	67.000	-23.528	25.550	1.00	25.31	1574	C VAL A 321	78.113	-21.225	37.192	1.00	24.11
1530	CB	SER A 314	66.307	-23.804	22.843	1.00	27.03	1575	O VAL A 321	78.998	-22.018	36.899	1.00	23.74
1531	OG	SER A 314	66.672	-25.175	22.739	1.00	28.18	1576	CB VAL A 321	76.477	-22.041	35.464	1.00	24.06
1532	N	GLY A 315	69.182	-23.694	25.070	1.00	24.12	1577	CG1 VAL A 321	75.861	-23.044	36.476	1.00	25.33
1533	CA	GLY A 315	69.527	-24.093	26.451	1.00	24.72	1578	CG2 VAL A 321	75.396	-21.628	34.452	1.00	23.25
1534	C	GLY A 315	69.338	-22.967	27.453	1.00	25.47	1579	N TYR A 322	78.040	-20.600	38.364	1.00	24.47
1535	O	GLY A 315	69.165	-21.816	27.048	1.00	26.04	1580	CA TYR A 322	79.021	-20.745	39.416	1.00	26.10
1536	N	ASN A 316	69.339	-23.228	28.754	1.00	25.24	1581	C TYR A 322	78.764	-21.897	40.382	1.00	26.90
1537	CA	ASN A 316	69.116	-22.249	29.805	1.00	25.73	1582	O TYR A 322	77.658	-22.184	40.816	1.00	25.89
1538	C	ASN A 316	70.297	-21.804	30.509	1.00	25.95	1583	CB TYR A 322	79.122	-19.432	40.251	1.00	25.11
1539	O	ASN A 316	70.298	-21.278	31.638	1.00	24.29	1584	CG TYR A 322	79.911	-19.624	41.541	1.00	25.40
1540	CB	ASN A 316	68.190	-22.893	30.866	1.00	29.42	1585	CD1 TYR A 322	81.291	-19.576	41.519	1.00	25.69
1541	CG	ASN A 316	68.861	-23.980	31.705	1.00	33.78	1586	CD2 TYR A 322	79.282	-19.866	42.764	1.00	25.12
1542	OD1	ASN A 316	70.048	-24.341	31.528	1.00	33.72	1587	CE1 TYR A 322	82.037	-19.772	42.669	1.00	26.68
1543	ND2	ASN A 316	68.154	-24.553	32.687	1.00	34.41	1588	CE2 TYR A 322	80.010	-20.046	43.920	1.00	26.18
1544	N	ASP A 317	71.584	-22.038	29.911	1.00	21.74	1589	CZ TYR A 322	81.383	-19.999	43.871	1.00	26.75
1545	CA	ASP A 317	72.807	-21.719	30.606	1.00	21.65	1590	OH TYR A 322	82.145	-20.197	44.987	1.00	27.96
1546	C	ASP A 317	73.650	-20.592	30.037	1.00	22.99	1591	N SER A 323	79.858	-22.517	40.812	1.00	27.80
1547	O	ASP A 317	74.868	-20.599	30.297	1.00	22.74	1592	CA SER A 323	79.884	-23.498	41.882	1.00	28.44
1548	CB	ASP A 317	74.675	-23.009	30.705	1.00	22.71	1593	C SER A 323	81.291	-23.469	42.494	1.00	28.56
1549	CG	ASP A 317	73.063	-23.483	29.316	1.00	23.13	1594	O SER A 323	82.252	-22.944	41.901	1.00	26.33
1550	OD1	ASP A 317	73.271	-23.346	28.363	1.00	22.02	1595	CB SER A 323	79.467	-24.897	41.536	1.00	27.55
1551	OD2	ASP A 317	75.185	-24.003	29.157	1.00	22.43	1596	OG SER A 323	80.342	-25.551	40.633	1.00	29.60
1552	N	LEU A 318	73.097	-19.656	29.260	1.00	22.59	1597	N LYS A 324	81.399	-24.048	43.683	1.00	29.32
1553	CA	LEU A 318	73.889	-18.531	28.754	1.00	20.66	1598	CA LYS A 324	82.674	-24.064	44.394	1.00	31.61
1554	C	LEU A 318	74.316	-17.676	29.955	1.00	20.42	1599	C LYS A 324	83.804	-24.679	43.609	1.00	30.15
1555	O	LEU A 318	73.547	-17.564	30.903	1.00	17.61	1600	O LYS A 324	84.882	-24.101	43.574	1.00	29.36
1556	CB	LEU A 318	73.169	-17.678	27.715	1.00	20.60	1601	CB LYS A 324	82.529	-24.863	45.697	1.00	35.71
1557	CG	LEU A 318	72.798	-18.391	26.385	1.00	19.68	1602	CG LYS A 324	82.413	-23.989	46.937	1.00	40.11
1558	CD1	LEU A 318	71.963	-17.493	25.495	1.00	17.29	1603	CD LYS A 324	82.177	-24.926	48.134	1.00	42.85
1559	CD2	LEU A 318	74.109	-18.776	25.680	1.00	16.96	1604	CE LYS A 324	80.695	-25.015	48.452	1.00	44.71
1560	N	GLY A 319	75.550	-17.187	29.890	1.00	20.73	1605	NZ LYS A 324	80.253	-23.993	49.436	1.00	46.25
1561	CA	GLY A 319	76.193	-16.428	30.949	1.00	20.43	1606	N ASP A 325	83.595	-25.836	42.979	1.00	30.61
1562	C	GLY A 319	77.202	-17.295	31.721	1.00	22.10	1607	CA ASP A 325	84.674	-26.467	42.219	1.00	31.24
1563	O	GLY A 319	77.914	-18.124	31.117	1.00	21.40	1608	C ASP A 325	84.934	-25.989	40.810	1.00	30.11
1564	N	ASN A 320	77.286	-17.098	33.042	1.00	19.98	1609	O ASP A 325	86.033	-26.273	40.306	1.00	28.10
1565	CA	ASN A 320	78.191	-17.952	33.835	1.00	21.91	1610	CB ASP A 325	84.425	-27.990	42.162	1.00	34.10
1566	C	ASN A 320	77.375	-18.729	34.867	1.00	22.53	1611	CG ASP A 325	84.438	-28.490	43.607	1.00	38.46
1567	O	ASN A 320	76.333	-18.231	35.331	1.00	21.27	1612	OD1 ASP A 325	85.027	-27.884	44.523	1.00	39.44
1568	CB	ASN A 320	79.297	-17.159	34.508	1.00	21.04	1613	OD2 ASP A 325	83.746	-29.499	43.857	1.00	40.94
1569	CG	ASN A 320	78.807	-16.191	35.571	1.00	21.93	1614	N ALA A 326	84.007	-25.274	40.168	1.00	26.93
1570	OD1	ASN A 320	78.574	-16.655	36.580	1.00	22.62	1615	CA ALA A 326	84.226	-2.816	38.800	1.00	24.07

1616	C	ALA A 326	83.169	-23.821	38.324	1.00	23.18	1661	N	TRP A 332	76.561	-16.576	22.985	1.00	17.30
1617	O	ALA A 326	82.044	-23.822	38.845	1.00	23.26	1662	CA	TRP A 332	76.128	-16.832	21.606	1.00	16.55
1618	CB	ALA A 326	84.066	-26.016	37.844	1.00	25.03	1663	C	TRP A 332	76.872	-15.925	20.635	1.00	16.29
1619	N	THR A 327	83.521	-23.011	37.326	1.00	22.27	1664	O	TRP A 332	76.594	-14.711	20.747	1.00	16.81
1620	CA	THR A 327	82.521	-22.114	36.751	1.00	22.23	1665	CB	TRP A 332	74.607	-16.801	21.475	1.00	15.95
1621	C	THR A 327	82.410	-22.371	35.241	1.00	23.00	1666	CG	TRP A 332	73.976	-17.064	20.126	1.00	16.61
1622	O	THR A 327	83.464	-22.441	34.587	1.00	22.16	1667	CD1	TRP A 332	73.873	-18.291	19.532	1.00	16.92
1623	CB	THR A 327	82.822	-20.630	36.971	1.00	22.19	1668	CD2	TRP A 332	73.332	-16.134	19.237	1.00	16.47
1624	OG1	THR A 327	82.652	-20.444	38.359	1.00	20.51	1669	NE1	TRP A 332	73.231	-18.170	18.311	1.00	18.27
1625	CG2	THR A 327	81.815	-19.716	36.226	1.00	21.57	1670	CE2	TRP A 332	72.866	-16.865	18.119	1.00	17.73
1626	N	SER A 328	81.189	-22.495	34.728	1.00	20.66	1671	CE3	TRP A 332	73.178	-14.747	19.217	1.00	16.21
1627	CA	SER A 328	81.065	-22.697	33.273	1.00	21.04	1672	CZ2	TRP A 332	72.274	-16.256	17.010	1.00	16.41
1628	C	SER A 328	80.570	-21.437	32.555	1.00	21.82	1673	CZ3	TRP A 332	72.531	-14.138	18.143	1.00	16.52
1629	O	SER A 328	79.704	-20.724	33.080	1.00	20.39	1674	CH2	TRP A 332	72.075	-14.905	17.057	1.00	15.60
1630	CB	SER A 328	80.013	-23.762	33.010	1.00	22.57	1675	N	ALA A 333	77.714	-16.446	19.737	1.00	16.60
1631	OG	SER A 328	80.420	-25.021	33.487	1.00	26.12	1676	CA	ALA A 333	78.444	-15.553	18.786	1.00	17.43
1632	N	PHE A 329	81.055	-21.187	31.335	1.00	20.94	1677	C	ALA A 333	78.657	-16.275	17.466	1.00	17.33
1633	CA	PHE A 329	80.703	-19.990	30.587	1.00	19.32	1678	O	ALA A 333	79.767	-16.726	17.165	1.00	17.44
1634	C	PHE A 329	80.108	-20.361	29.232	1.00	20.62	1679	CB	ALA A 333	79.803	-15.187	19.395	1.00	17.32
1635	O	PHE A 329	80.520	-21.374	28.618	1.00	18.58	1680	N	PRO A 334	77.615	-16.422	16.640	1.00	16.81
1636	CB	PHE A 329	81.937	-19.097	30.414	1.00	17.82	1681	CA	PRO A 334	77.667	-17.222	15.426	1.00	16.90
1637	CG	PHE A 329	82.637	-18.648	31.677	1.00	19.59	1682	C	PRO A 334	78.499	-16.717	14.264	1.00	18.01
1638	CD1	PHE A 329	83.556	-19.478	32.308	1.00	16.87	1683	O	PRO A 334	78.812	-17.501	13.340	1.00	19.09
1639	CD2	PHE A 329	82.377	-17.385	32.209	1.00	19.26	1684	CB	PRO A 334	76.165	-17.379	15.095	1.00	17.28
1640	CE1	PHE A 329	84.195	-19.074	33.465	1.00	19.15	1685	CG	PRO A 334	75.567	-16.049	15.533	1.00	17.13
1641	CE2	PHE A 329	83.064	-16.954	33.344	1.00	18.66	1686	CD	PRO A 334	76.259	-15.842	16.881	1.00	15.63
1642	CZ	PHE A 329	83.904	-17.819	33.995	1.00	19.30	1687	N	THR A 335	78.966	-15.478	14.258	1.00	17.49
1643	N	ARG A 330	79.142	-19.576	28.754	1.00	19.04	1688	CA	THR A 335	79.765	-14.969	13.145	1.00	19.36
1644	CA	ARG A 330	78.571	-19.791	27.432	1.00	17.97	1689	C	THR A 335	81.245	-14.804	13.484	1.00	19.67
1645	C	ARG A 330	78.029	-18.474	26.858	1.00	19.63	1690	O	THR A 335	82.095	-14.363	12.681	1.00	19.24
1646	O	ARG A 330	77.319	-17.717	27.557	1.00	18.47	1691	CB	THR A 335	79.202	-13.632	12.595	1.00	19.04
1647	CB	ARG A 330	77.471	-20.860	27.393	1.00	20.74	1692	OG1	THR A 335	79.459	-12.557	13.518	1.00	18.31
1648	CG	ARG A 330	77.092	-21.262	25.948	1.00	21.20	1693	CG2	THR A 335	77.709	-13.744	12.268	1.00	18.55
1649	CD	ARG A 330	75.983	-22.295	25.893	1.00	21.96	1694	N	ALA A 336	81.589	-15.082	14.737	1.00	20.15
1650	NE	ARG A 330	76.296	-23.594	26.492	1.00	22.92	1695	CA	ALA A 336	82.961	-14.943	15.225	1.00	21.16
1651	CZ	ARG A 330	76.812	-24.638	25.839	1.00	23.47	1696	C	ALA A 336	83.915	-16.034	14.731	1.00	20.66
1652	NH1	ARG A 330	77.076	-25.760	26.503	1.00	23.14	1697	O	ALA A 336	83.522	-17.199	14.668	1.00	20.80
1653	NH2	ARG A 330	77.034	-24.625	24.528	1.00	20.70	1698	CB	ALA A 336	82.965	-15.048	16.765	1.00	19.61
1654	N	VAL A 331	78.421	-18.196	25.605	1.00	18.50	1699	N	SER A 337	85.164	-15.642	14.454	1.00	21.24
1655	CA	VAL A 331	77.991	-16.939	24.952	1.00	18.28	1700	CA	SER A 337	86.158	-16.646	14.033	1.00	21.72
1656	C	VAL A 331	77.605	-17.227	23.505	1.00	17.84	1701	C	SER A 337	86.913	-17.153	15.263	1.00	22.44
1657	O	VAL A 331	78.271	-18.081	22.888	1.00	17.02	1702	O	SER A 337	87.457	-18.262	15.262	1.00	22.33
1658	CB	VAL A 331	79.103	-15.885	25.030	1.00	17.74	1703	CB	SER A 337	87.101	-16.133	12.942	1.00	19.79
1659	CG1	VAL A 331	80.369	-16.391	24.320	1.00	18.41	1704	OG	SER A 337	87.842	-15.014	13.378	1.00	19.73
1660	CG2	VAL A 331	78.693	-14.550	24.422	1.00	18.27	1705	N	ASN A 338	86.800	-16.461	16.395	1.00	22.39

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1706	CA	ASN A 338	87.474	-16.897	17.629	1.00	22.59	1751	CD1	LEU A 343	89.386	-17.523	34.242	1.00	22.59
1707	C	ASN A 338	86.895	-16.133	18.822	1.00	21.70	1752	CD2	LEU A 343	87.574	-15.819	34.402	1.00	22.28
1708	O	ASN A 338	86.551	-14.961	18.662	1.00	20.21	1753	N	TTR A 344	90.187	-12.001	35.296	1.00	21.67
1709	CB	ASN A 338	88.985	-16.546	17.593	1.00	23.25	1754	CA	TTR A 344	90.891	-11.029	36.081	1.00	20.84
1710	CG	ASN A 338	89.769	-17.286	18.665	1.00	23.27	1755	C	TTR A 344	90.731	-11.309	37.578	1.00	22.98
1711	OD1	ASN A 338	89.309	-18.312	19.176	1.00	24.41	1756	O	TTR A 344	89.595	-11.488	38.042	1.00	20.73
1712	ND2	ASN A 338	90.949	-16.819	19.009	1.00	22.31	1757	CB	TTR A 344	90.471	-9.590	35.781	1.00	22.01
1713	N	VAL A 339	86.788	-16.750	19.982	1.00	20.64	1758	CG	TTR A 344	90.514	-9.119	34.350	1.00	22.91
1714	CA	VAL A 339	86.296	-16.110	21.195	1.00	20.93	1759	CD1	TTR A 344	89.464	-9.443	33.473	1.00	23.47
1715	C	VAL A 339	87.216	-16.633	22.325	1.00	21.76	1760	CD2	TTR A 344	91.589	-8.413	33.839	1.00	23.31
1716	O	VAL A 339	87.446	-17.852	22.405	1.00	20.76	1761	CE1	TTR A 344	89.503	-9.068	32.134	1.00	22.88
1717	CB	VAL A 339	84.849	-16.455	21.599	1.00	20.75	1762	CE2	TTR A 344	91.600	-7.977	32.516	1.00	24.05
1718	CG1	VAL A 339	84.446	-15.701	22.879	1.00	20.39	1763	C2	TTR A 344	90.574	-8.343	31.665	1.00	23.45
1719	CG2	VAL A 339	83.840	-16.157	20.492	1.00	20.29	1764	OH	TTR A 344	90.607	-7.928	30.344	1.00	21.39
1720	N	GLN A 340	87.759	-15.716	23.111	1.00	19.11	1765	N	ASN A 345	91.843	-11.311	38.344	1.00	23.99
1721	CA	GLN A 340	88.577	-16.086	24.253	1.00	21.95	1766	CA	ASN A 345	91.708	-11.557	39.793	1.00	26.27
1722	C	GLN A 340	87.972	-15.504	25.543	1.00	22.76	1767	C	ASN A 345	91.603	-10.255	40.558	1.00	26.36
1723	O	GLN A 340	87.332	-14.438	25.536	1.00	20.68	1768	O	ASN A 345	91.850	-10.193	41.752	1.00	28.06
1724	CB	GLN A 340	90.005	-15.531	24.024	1.00	25.09	1769	CB	ASN A 345	92.841	-12.427	40.366	1.00	27.33
1725	CG	GLN A 340	90.662	-16.091	22.738	1.00	28.48	1770	CG	ASN A 345	94.204	-11.783	40.253	1.00	27.96
1726	CD	GLN A 340	92.158	-15.840	22.679	1.00	32.41	1771	OD1	ASN A 345	94.333	-10.580	39.995	1.00	26.96
1727	OE1	GLN A 340	92.611	-14.980	21.913	1.00	34.76	1772	ND2	ASN A 345	95.254	-12.588	40.461	1.00	30.19
1728	NE2	GLN A 340	92.927	-16.566	23.479	1.00	32.06	1773	N	SER A 346	91.183	-9.172	39.904	1.00	27.11
1729	N	LEU A 341	88.203	-16.164	26.673	1.00	21.03	1774	CA	SER A 346	91.040	-7.885	40.569	1.00	26.45
1730	CA	LEU A 341	87.802	-15.701	27.996	1.00	19.98	1775	C	SER A 346	90.101	-7.018	39.745	1.00	26.06
1731	C	LEU A 341	88.980	-14.997	28.691	1.00	20.18	1776	O	SER A 346	89.895	-7.299	38.584	1.00	26.29
1732	O	LEU A 341	90.067	-15.556	28.788	1.00	18.71	1777	CB	SER A 346	92.413	-7.241	40.740	1.00	24.63
1733	CB	LEU A 341	87.383	-16.917	28.829	1.00	19.90	1778	OG	SER A 346	92.769	-6.551	39.569	1.00	23.97
1734	CG	LEU A 341	86.998	-16.678	30.295	1.00	21.43	1779	N	GLU A 347	89.587	-5.953	40.320	1.00	25.01
1735	CD1	LEU A 341	85.703	-15.837	30.345	1.00	20.84	1780	CA	GLU A 347	88.629	-5.103	39.610	1.00	26.48
1736	CD2	LEU A 341	86.828	-18.018	31.006	1.00	20.08	1781	C	GLU A 347	89.285	-4.207	38.593	1.00	27.56
1737	N	LEU A 342	88.796	-13.750	29.074	1.00	19.42	1782	O	GLU A 347	88.618	-3.846	37.608	1.00	26.07
1738	CA	LEU A 342	89.731	-12.963	29.842	1.00	21.69	1783	CB	GLU A 347	87.833	-4.290	40.665	1.00	26.52
1739	C	LEU A 342	89.252	-12.963	31.306	1.00	22.95	1784	CG	GLU A 347	86.563	-3.647	40.158	1.00	25.42
1740	O	LEU A 342	88.125	-12.555	31.641	1.00	21.27	1785	CD	GLU A 347	85.681	-3.082	41.265	1.00	25.59
1741	CB	LEU A 342	89.901	-11.557	29.277	1.00	22.45	1786	OE1	GLU A 347	84.477	-2.829	41.018	1.00	23.17
1742	CG	LEU A 342	90.120	-11.437	27.750	1.00	23.01	1787	OE2	GLU A 347	86.140	-2.884	42.416	1.00	24.63
1743	CD1	LEU A 342	90.324	-9.977	27.354	1.00	20.48	1788	N	LVS A 348	90.532	-3.758	38.843	1.00	27.94
1744	CD2	LEU A 342	91.270	-12.283	27.239	1.00	24.22	1789	CA	LVS A 348	91.239	-2.907	37.892	1.00	30.23
1745	N	LEU A 343	90.090	-13.551	32.167	1.00	21.42	1790	C	LVS A 348	92.602	-3.443	37.434	1.00	30.18
1746	CA	LEU A 343	89.834	-13.675	33.594	1.00	22.82	1791	O	LVS A 348	93.183	-2.871	36.515	1.00	30.31
1747	C	LEU A 343	90.771	-12.755	34.359	1.00	23.56	1792	CB	LVS A 348	91.496	-1.484	38.403	1.00	32.74
1748	O	LEU A 343	91.973	-12.618	34.049	1.00	22.34	1793	CG	LVS A 348	90.350	-0.740	39.058	1.00	36.60
1749	CB	LEU A 343	89.977	-15.095	34.112	1.00	23.13	1794	CD	LVS A 348	90.397	-0.890	40.579	1.00	39.69
1750	CG	LEU A 343	88.936	-16.134	33.765	1.00	24.04	1795	CR	LVS A 348	91.755	-0.453	41.157	1.00	40.78

1796	NZ	LYS A 348	91.956	-0.820	42.572	1.00	40.05	1841	CA	LEU A 355	91.935	-18.815	27.630	1.00	25.52
1797	N	GLY A 349	93.121	-4.508	38.002	1.00	29.40	1842	C	LEU A 355	91.099	-18.933	26.358	1.00	25.60
1798	CA	GLY A 349	94.413	-5.069	37.659	1.00	30.15	1843	O	LEU A 355	90.052	-18.276	26.296	1.00	23.63
1799	C	GLY A 349	94.469	-5.699	36.268	1.00	29.96	1844	CB	LEU A 355	91.104	-19.459	28.763	1.00	23.98
1800	O	GLY A 349	93.436	-5.955	35.630	1.00	26.44	1845	CG	LEU A 355	91.678	-20.180	29.957	1.00	27.14
1801	N	SR A 350	95.695	-5.979	35.812	1.00	27.06	1846	CD1	LEU A 355	93.202	-20.110	30.090	1.00	24.35
1802	CA	SR A 350	95.884	-6.505	34.472	1.00	26.80	1847	CD2	LEU A 355	91.046	-19.801	31.294	1.00	24.19
1803	C	SR A 350	95.470	-7.962	34.377	1.00	27.11	1848	N	GLU A 356	91.388	-19.914	25.498	1.00	24.90
1804	O	SR A 350	95.237	-8.656	35.366	1.00	26.51	1849	CA	GLU A 356	90.561	-20.149	24.328	1.00	25.07
1805	CB	SR A 350	97.333	-6.250	33.997	1.00	28.64	1850	C	GLU A 356	89.240	-20.795	24.749	1.00	24.27
1806	OG	SR A 350	98.234	-7.164	34.581	1.00	25.07	1851	O	GLU A 356	89.220	-21.728	25.556	1.00	24.57
1807	N	ILE A 351	95.238	-8.418	33.148	1.00	27.83	1852	CB	GLU A 356	91.263	-21.110	23.354	1.00	26.34
1808	CA	ILE A 351	94.751	-9.754	32.873	1.00	27.61	1853	CG	GLU A 356	92.307	-20.425	22.486	1.00	28.70
1809	C	ILE A 351	95.544	-10.819	33.604	1.00	28.09	1854	CD	GLU A 356	91.664	-19.583	21.391	1.00	29.91
1810	O	ILE A 351	96.782	-10.849	33.632	1.00	25.86	1855	OE1	GLU A 356	90.508	-19.768	20.973	1.00	30.84
1811	CB	ILE A 351	94.698	-10.042	31.362	1.00	30.70	1856	OE2	GLU A 356	92.360	-18.651	20.957	1.00	31.88
1812	CG1	ILE A 351	94.270	-11.501	31.097	1.00	30.30	1857	N	MET A 357	88.138	-20.398	24.144	1.00	24.03
1813	CG2	ILE A 351	96.082	-9.848	30.749	1.00	32.44	1858	CA	MET A 357	86.839	-21.025	24.390	1.00	21.73
1814	CD1	ILE A 351	93.598	-11.582	29.747	1.00	33.45	1859	C	MET A 357	86.645	-22.023	23.268	1.00	22.56
1815	N	THR A 352	94.804	-11.747	34.211	1.00	26.74	1860	O	MET A 357	87.422	-21.932	22.306	1.00	23.10
1816	CA	THR A 352	95.382	-12.823	34.980	1.00	27.48	1861	CB	MET A 357	85.724	-19.974	24.468	1.00	20.62
1817	C	THR A 352	95.555	-14.073	34.136	1.00	28.86	1862	CG	MET A 357	85.893	-19.016	25.636	1.00	19.78
1818	O	THR A 352	96.539	-14.780	34.332	1.00	29.06	1863	SD	MET A 357	84.518	-17.881	25.954	1.00	18.56
1819	CB	THR A 352	94.507	-13.196	36.212	1.00	26.13	1864	CE	MET A 357	83.209	-19.002	26.424	1.00	17.50
1820	OG1	THR A 352	94.336	-11.981	36.927	1.00	25.38	1865	N	GLN A 358	85.749	-22.969	23.351	1.00	23.45
1821	CG2	THR A 352	95.178	-14.198	37.140	1.00	27.23	1866	CA	GLN A 358	85.504	-23.939	22.312	1.00	26.55
1822	N	LYS A 353	94.575	-14.379	33.308	1.00	28.99	1867	C	GLN A 358	84.150	-23.684	21.603	1.00	25.08
1823	CA	LYS A 353	94.536	-15.603	32.517	1.00	31.07	1868	O	GLN A 358	83.110	-23.528	22.253	1.00	21.83
1824	C	LYS A 353	93.738	-15.337	31.224	1.00	31.82	1869	CB	GLN A 358	85.324	-25.373	22.847	1.00	29.06
1825	O	LYS A 353	92.623	-14.771	31.223	1.00	26.80	1870	CG	GLN A 358	85.931	-26.928	24.804	1.00	38.87
1826	CB	LYS A 353	93.848	-16.644	33.383	1.00	34.73	1871	CD	GLN A 358	85.386	-27.019	26.035	1.00	42.16
1827	CG	LYS A 353	94.468	-17.997	33.598	1.00	40.91	1872	OE1	GLN A 358	84.727	-27.807	23.987	1.00	40.44
1828	CD	LYS A 353	93.462	-19.025	34.085	1.00	44.90	1873	NE2	GLN A 358	84.197	-23.798	20.304	1.00	24.04
1829	CE	LYS A 353	93.470	-19.297	35.585	1.00	47.03	1874	N	LYS A 359	83.007	-23.709	19.465	1.00	26.25
1830	NZ	LYS A 353	92.210	-20.014	35.986	1.00	47.57	1875	CA	LYS A 359	82.043	-24.816	19.852	1.00	24.84
1831	N	GLN A 354	94.323	-15.729	30.091	1.00	29.04	1876	C	LYS A 359	82.493	-25.956	19.974	1.00	26.59
1832	CA	GLN A 354	93.676	-15.609	28.795	1.00	29.05	1877	O	LYS A 359	83.343	-23.834	17.978	1.00	26.51
1833	C	GLN A 354	93.487	-17.017	28.238	1.00	30.10	1878	CB	LYS A 359	82.110	-23.602	17.112	1.00	29.91
1834	O	GLN A 354	94.488	-17.758	28.103	1.00	31.21	1879	CG	LYS A 359	81.361	-22.329	17.504	1.00	30.23
1835	CB	GLN A 354	94.467	-14.688	27.880	1.00	29.18	1880	CD	LYS A 359	79.954	-22.267	16.933	1.00	28.64
1836	CG	GLN A 354	93.905	-14.566	26.477	1.00	31.51	1881	CE	LYS A 359	80.031	-22.364	15.441	1.00	28.49
1837	CD	GLN A 354	94.412	-13.380	25.699	1.00	35.08	1882	NZ	LYS A 359	79.794	-25.489	20.549	1.00	23.71
1838	OE1	GLN A 354	94.375	-13.338	24.466	1.00	37.15	1883	N	SER A 360	78.515	-25.385	19.738	1.00	24.86
1839	NE2	GLN A 354	94.905	-12.320	26.329	1.00	37.06	1884	CA	SER A 360					
1840	N	LEU A 355	92.253	-17.454	28.014	1.00	25.86	1885	C	SER A 360					

1976	O	ASN A 372	87.724	-19.265	42.643	1.00	28.03	2021	CA	TYR A 377	86.016	-10.505	37.051	1.00	19.50
1977	CB	ASN A 372	86.716	-21.406	44.286	1.00	33.96	2022	C	TYR A 377	86.358	-11.145	35.703	1.00	20.68
1978	CG	ASN A 372	85.534	-20.773	44.992	1.00	36.29	2023	O	TYR A 377	87.330	-11.914	35.605	1.00	19.41
1979	OD1	ASN A 372	84.864	-19.865	44.493	1.00	35.90	2024	CB	TYR A 377	86.409	-9.027	37.144	1.00	17.91
1980	ND2	ASN A 372	85.211	-21.241	46.212	1.00	35.53	2025	CG	TYR A 377	85.956	-8.348	38.427	1.00	18.83
1981	N	LEU A 373	85.865	-19.526	41.377	1.00	25.26	2026	CD1	TYR A 377	86.708	-8.461	39.604	1.00	19.72
1982	CA	LEU A 373	86.006	-18.204	40.775	1.00	23.40	2027	CD2	TYR A 377	84.808	-7.586	38.514	1.00	17.93
1983	C	LEU A 373	85.148	-17.151	41.456	1.00	22.75	2028	CE1	TYR A 377	86.334	-7.877	40.796	1.00	18.37
1984	O	LEU A 373	84.924	-16.071	40.902	1.00	20.78	2029	CE2	TYR A 377	84.394	-6.978	39.692	1.00	17.34
1985	CB	LEU A 373	85.754	-18.243	39.260	1.00	23.70	2030	CZ	TYR A 377	85.181	-7.130	40.849	1.00	20.22
1986	CG	LEU A 373	86.733	-19.077	38.413	1.00	24.26	2031	OH	TYR A 377	84.783	-6.517	42.039	1.00	15.40
1987	CD1	LEU A 373	86.538	-18.827	36.918	1.00	24.86	2032	N	TYR A 378	85.628	-10.823	34.626	1.00	20.04
1988	CD2	LEU A 373	88.185	-18.745	38.729	1.00	26.18	2033	CA	TYR A 378	85.785	-11.425	33.337	1.00	19.08
1989	N	GLU A 374	84.705	-17.422	42.691	1.00	22.76	2034	C	TYR A 378	85.235	-10.613	32.166	1.00	19.99
1990	CA	GLU A 374	83.955	-16.376	43.386	1.00	20.88	2035	O	TYR A 378	84.354	-9.760	32.334	1.00	20.17
1991	C	GLU A 374	84.658	-15.013	43.353	1.00	21.01	2036	CB	TYR A 378	85.171	-12.819	33.281	1.00	18.87
1992	O	GLU A 374	85.868	-14.894	43.493	1.00	18.90	2037	CG	TYR A 378	83.675	-13.049	33.109	1.00	19.44
1993	CB	GLU A 374	83.722	-16.806	44.835	1.00	23.51	2038	CD1	TYR A 378	83.148	-13.529	31.906	1.00	17.38
1994	CG	GLU A 374	82.766	-15.862	45.565	1.00	25.57	2039	CD2	TYR A 378	82.794	-12.845	34.175	1.00	17.88
1995	CD	GLU A 374	82.144	-16.577	46.741	1.00	29.28	2040	CE1	TYR A 378	81.784	-13.770	31.768	1.00	18.82
1996	OE1	GLU A 374	82.604	-17.557	47.084	1.00	29.30	2041	CE2	TYR A 378	81.431	-13.071	34.036	1.00	18.35
1997	OE2	GLU A 374	81.193	-16.042	47.307	1.00	27.72	2042	CZ	TYR A 378	80.926	-13.553	32.837	1.00	17.91
1998	N	ASN A 375	83.841	-13.965	43.118	1.00	19.21	2043	OH	TYR A 378	79.558	-13.797	32.732	1.00	18.43
1999	CA	ASN A 375	84.357	-12.596	43.101	1.00	19.30	2044	N	LEU A 379	85.839	-10.897	30.993	1.00	17.82
2000	C	ASN A 375	85.512	-12.400	42.116	1.00	19.99	2045	CA	LEU A 379	85.409	-10.274	29.738	1.00	17.08
2001	O	ASN A 375	86.381	-11.553	42.288	1.00	18.96	2046	C	LEU A 379	85.510	-11.341	28.635	1.00	15.93
2002	CB	ASN A 375	84.810	-12.224	44.515	1.00	21.23	2047	O	LEU A 379	86.145	-12.370	28.873	1.00	15.93
2003	CG	ASN A 375	83.658	-12.390	45.469	1.00	22.98	2048	CB	LEU A 379	86.246	-9.088	29.300	1.00	17.38
2004	OD1	ASN A 375	83.828	-12.711	46.642	1.00	21.72	2049	CG	LEU A 379	86.193	-7.747	30.010	1.00	19.69
2005	ND2	ASN A 375	82.446	-12.157	44.937	1.00	19.08	2050	CD1	LEU A 379	87.317	-6.812	29.589	1.00	16.36
2006	N	TRP A 376	85.534	-13.250	41.077	1.00	18.63	2051	CD2	LEU A 379	84.837	-7.062	29.750	1.00	18.77
2007	CA	TRP A 376	86.479	-13.023	39.991	1.00	20.31	2052	N	TYR A 380	84.730	-11.180	27.547	1.00	19.37
2008	C	TRP A 376	85.908	-12.050	38.948	1.00	20.90	2053	CA	TYR A 380	84.862	-12.039	26.387	1.00	19.03
2009	O	TRP A 376	84.705	-11.885	38.809	1.00	20.95	2054	C	TYR A 380	85.691	-11.243	25.346	1.00	19.03
2010	CB	TRP A 376	86.796	-14.374	39.348	1.00	21.71	2055	O	TYR A 380	85.468	-10.031	25.169	1.00	17.35
2011	CG	TRP A 376	87.964	-15.000	40.012	1.00	22.49	2056	CB	TYR A 380	83.558	-12.495	25.715	1.00	17.93
2012	CD1	TRP A 376	88.036	-15.457	41.347	1.00	20.13	2057	CG	TYR A 380	82.665	-13.391	26.562	1.00	17.93
2013	CD2	TRP A 376	89.290	-15.156	39.450	1.00	22.92	2058	CD1	TYR A 380	81.332	-13.060	26.782	1.00	17.57
2014	NE1	TRP A 376	89.280	-15.887	41.683	1.00	20.87	2059	CD2	TYR A 380	83.146	-14.541	27.170	1.00	16.75
2015	CE2	TRP A 376	90.116	-15.690	40.471	1.00	22.98	2060	CE1	TYR A 380	80.485	-13.866	27.548	1.00	18.52
2016	CE3	TRP A 376	89.839	-14.871	38.203	1.00	23.59	2061	CE2	TYR A 380	82.344	-15.343	27.948	1.00	17.90
2017	CZ2	TRP A 376	91.464	-15.903	40.230	1.00	23.06	2062	CZ	TYR A 380	81.011	-15.013	28.134	1.00	17.98
2018	CZ3	TRP A 376	91.187	-15.088	37.962	1.00	24.45	2063	OH	TYR A 380	80.229	-15.823	28.913	1.00	16.91
2019	CH2	TRP A 376	92.005	-15.606	38.983	1.00	23.52	2064	N	GLN A 381	86.621	-11.910	24.682	1.00	18.61
2020	N	TYR A 377	86.618	-11.303	38.111	1.00	19.49	2065	CA	GLN A 381	87.401	-11.198	23.645	1.00	19.39

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2246	NH1 ARG A 405	90.555	-6.060	36.027	1.00	17.06	2291	N	LXS A 412	73.415	-17.079	46.331	1.00	21.58
2247	NH2 ARG A 405	91.142	-4.729	34.232	1.00	19.62	2292	CA	LXS A 412	72.795	-17.452	47.612	1.00	22.40
2248	N GLY A 406	82.544	-7.922	33.884	1.00	15.61	2293	C	LXS A 412	73.254	-16.679	48.824	1.00	22.02
2249	CA GLY A 406	81.431	-8.620	34.562	1.00	16.45	2294	O	LXS A 412	72.506	-16.191	49.703	1.00	22.52
2250	C GLY A 406	82.102	-9.320	35.780	1.00	18.96	2295	CB	LXS A 412	73.028	-18.966	47.842	1.00	26.92
2251	O GLY A 406	83.334	-9.449	35.807	1.00	16.60	2296	CG	LXS A 412	72.311	-19.472	49.084	1.00	31.49
2252	N MET A 407	81.317	-9.686	36.773	1.00	18.47	2297	CD	LXS A 412	70.825	-19.669	48.788	1.00	33.84
2253	CA MET A 407	81.762	-10.295	38.010	1.00	18.88	2298	CE	LXS A 412	70.110	-19.953	50.118	1.00	37.42
2254	C MET A 407	81.015	-11.578	38.326	1.00	18.40	2299	NZ	LXS A 412	70.382	-18.751	50.970	1.00	40.45
2255	O MET A 407	79.775	-11.615	38.240	1.00	17.72	2300	N	ALA A 413	74.517	-16.248	48.810	1.00	18.93
2256	CB MET A 407	81.542	-9.323	39.182	1.00	18.65	2301	CA	ALA A 413	75.194	-15.455	49.803	1.00	20.77
2257	CG MET A 407	82.166	-9.673	40.526	1.00	16.86	2302	C	ALA A 413	74.716	-14.003	49.860	1.00	20.66
2258	SD MET A 407	81.647	-8.523	41.829	1.00	19.73	2303	O	ALA A 413	74.909	-13.273	50.842	1.00	21.58
2259	CE MET A 407	82.557	-9.127	43.234	1.00	17.44	2304	CB	ALA A 413	76.696	-15.412	49.507	1.00	19.90
2260	N ILE A 408	81.750	-12.645	38.616	1.00	16.52	2305	N	THR A 414	74.083	-13.550	48.779	1.00	19.42
2261	CA ILE A 408	81.201	-13.950	38.956	1.00	14.94	2306	CA	THR A 414	73.566	-12.207	48.706	1.00	20.42
2262	C ILE A 408	80.888	-13.997	40.454	1.00	18.17	2307	C	THR A 414	72.181	-12.039	49.330	1.00	22.20
2263	O ILE A 408	81.786	-13.697	41.268	1.00	19.12	2308	O	THR A 414	71.750	-10.883	49.514	1.00	20.49
2264	CB ILE A 408	82.249	-15.018	38.606	1.00	15.45	2309	CB	THR A 414	73.489	-11.665	47.263	1.00	20.49
2265	CG1 ILE A 408	82.565	-15.005	37.081	1.00	15.33	2310	CG1	THR A 414	72.430	-12.401	46.619	1.00	21.35
2266	CG2 ILE A 408	81.742	-16.389	39.050	1.00	16.59	2311	CG2	THR A 414	74.770	-11.821	46.451	1.00	19.00
2267	CD1 ILE A 408	84.051	-15.308	36.771	1.00	17.24	2312	N	ASP A 415	71.470	-13.097	49.627	1.00	21.64
2268	N VAL A 409	79.647	-14.260	40.875	1.00	16.48	2313	CA	ASP A 415	70.149	-13.115	50.208	1.00	21.34
2269	CA VAL A 409	79.309	-14.206	42.292	1.00	18.09	2314	C	ASP A 415	70.129	-12.642	51.661	1.00	20.48
2270	C VAL A 409	78.466	-15.386	42.736	1.00	19.37	2315	O	ASP A 415	70.955	-13.100	52.457	1.00	21.23
2271	O VAL A 409	77.906	-16.108	41.930	1.00	20.30	2316	CB	ASP A 415	69.544	-14.522	50.278	1.00	21.16
2272	CB VAL A 409	78.544	-12.920	42.668	1.00	17.54	2317	CG	ASP A 415	69.327	-15.177	48.937	1.00	23.55
2273	CG1 VAL A 409	79.352	-11.657	42.436	1.00	14.93	2318	OD1	ASP A 415	69.131	-14.545	47.881	1.00	22.11
2274	CG2 VAL A 409	77.237	-12.727	41.871	1.00	18.02	2319	OD2	ASP A 415	69.342	-16.414	48.905	1.00	24.37
2275	N ASP A 410	78.372	-15.587	44.041	1.00	21.46	2320	N	PRO A 416	69.298	-11.654	51.921	1.00	18.99
2276	CA ASP A 410	77.548	-16.630	44.651	1.00	23.20	2321	CA	PRO A 416	69.131	-11.131	53.268	1.00	18.59
2277	C ASP A 410	76.213	-15.995	45.035	1.00	22.82	2322	C	PRO A 416	68.487	-12.203	54.143	1.00	19.83
2278	O ASP A 410	76.182	-15.290	46.065	1.00	22.94	2323	O	PRO A 416	67.848	-13.131	53.613	1.00	16.95
2279	CB ASP A 410	78.239	-17.131	45.946	1.00	23.65	2324	CB	PRO A 416	68.177	-9.955	53.092	1.00	18.50
2280	CG ASP A 410	77.474	-18.262	46.611	1.00	24.86	2325	CG	PRO A 416	67.383	-10.255	51.848	1.00	18.19
2281	OD1 ASP A 410	76.311	-18.535	46.249	1.00	25.50	2326	CD	PRO A 416	68.355	-11.017	50.963	1.00	18.15
2282	OD2 ASP A 410	78.060	-18.934	47.490	1.00	27.15	2327	N	ALA A 417	68.584	-12.001	55.459	1.00	19.41
2283	N LEU A 411	75.146	-16.167	44.271	1.00	21.42	2328	CA	ALA A 417	67.928	-12.898	56.410	1.00	18.88
2284	CA LEU A 411	73.882	-15.508	44.506	1.00	21.38	2329	C	ALA A 417	66.416	-12.866	56.226	1.00	19.84
2285	C LEU A 411	71.237	-15.851	45.845	1.00	22.44	2330	O	ALA A 417	65.795	-11.828	55.964	1.00	19.83
2286	O LEU A 411	72.566	-14.989	46.436	1.00	19.95	2331	CB	ALA A 417	68.258	-12.437	57.822	1.00	18.37
2287	CB LEU A 411	72.876	-15.820	43.360	1.00	20.60	2332	N	GLY A 418	65.790	-14.020	56.379	1.00	21.41
2288	CG LEU A 411	73.222	-15.156	42.010	1.00	20.02	2333	CA	GLY A 418	64.368	-14.233	56.237	1.00	23.22
2289	CD1 LEU A 411	72.363	-15.723	40.902	1.00	16.46	2334	C	GLY A 418	63.846	-14.337	54.810	1.00	23.60
2290	CD2 LEU A 411	73.133	-13.644	42.152	1.00	19.54	2335	O	GLY A 418	62.643	-14.572	54.590	1.00	22.08

2336	N	TRP	A	419	64.710	-14.183	53.807	1.00	23.46	2381	N	GLU	A	424	55.414	-13.228	47.961	1.00	43.93
2337	CA	TRP	A	419	64.402	-14.234	52.396	1.00	23.20	2382	CA	GLU	A	424	54.955	-12.662	46.717	1.00	41.46
2338	C	TRP	A	419	63.606	-15.472	52.012	1.00	25.42	2383	C	GLU	A	424	53.561	-12.097	47.029	1.00	35.89
2339	O	TRP	A	419	62.668	-15.373	51.199	1.00	24.03	2384	O	GLU	A	424	52.765	-12.666	47.764	1.00	32.50
2340	CB	TRP	A	419	65.670	-14.233	51.530	1.00	22.84	2385	CB	GLU	A	424	54.860	-13.614	45.537	1.00	45.39
2341	CG	TRP	A	419	65.454	-13.984	50.043	1.00	22.68	2386	CG	GLU	A	424	53.602	-14.436	45.385	1.00	50.15
2342	CD1	TRP	A	419	65.788	-14.816	48.989	1.00	21.27	2387	CD	GLU	A	424	53.588	-15.845	45.929	1.00	53.14
2343	CD2	TRP	A	419	64.806	-12.860	49.459	1.00	20.14	2388	OE1	GLU	A	424	52.472	-16.435	45.889	1.00	55.07
2344	NE1	TRP	A	419	65.454	-14.166	47.813	1.00	20.72	2389	OE2	GLU	A	424	54.628	-16.378	46.392	1.00	54.61
2345	CE2	TRP	A	419	64.841	-12.969	48.060	1.00	21.05	2390	N	GLN	A	425	53.341	-10.927	46.478	1.00	31.51
2346	CE3	TRP	A	419	64.233	-11.704	50.009	1.00	21.41	2391	CA	GLN	A	425	52.114	-10.187	46.730	1.00	30.43
2347	CZ2	TRP	A	419	64.305	-12.027	47.163	1.00	20.75	2392	C	GLN	A	425	51.336	-9.895	45.465	1.00	27.84
2348	CZ3	TRP	A	419	63.711	-10.769	49.147	1.00	22.68	2393	O	GLN	A	425	51.444	-8.806	44.889	1.00	25.73
2349	CH2	TRP	A	419	63.761	-10.889	47.753	1.00	21.75	2394	CB	GLN	A	425	52.513	-8.862	47.412	1.00	28.91
2350	N	GLN	A	420	63.929	-16.638	52.581	1.00	26.47	2395	CG	GLN	A	425	52.923	-9.100	48.863	1.00	31.80
2351	CA	GLN	A	420	63.179	-17.861	52.325	1.00	29.80	2396	CD	GLN	A	425	51.701	-9.408	49.711	1.00	34.90
2352	C	GLN	A	420	61.719	-17.770	52.728	1.00	28.92	2397	OE1	GLN	A	425	51.857	-10.238	50.604	1.00	35.50
2353	O	GLN	A	420	60.919	-18.452	52.090	1.00	28.66	2398	NE2	GLN	A	425	50.583	-8.779	49.384	1.00	34.92
2354	CB	GLN	A	420	63.849	-19.089	52.961	1.00	33.14	2399	N	THR	A	426	50.650	-10.924	44.981	1.00	25.79
2355	CG	GLN	A	420	64.919	-19.737	52.090	1.00	39.56	2400	CA	THR	A	426	49.878	-10.700	43.722	1.00	25.43
2356	CD	GLN	A	420	64.607	-19.919	50.614	1.00	41.28	2401	C	THR	A	426	48.194	-12.077	44.673	1.00	25.67
2357	OE1	GLN	A	420	65.071	-19.074	49.835	1.00	43.54	2402	O	THR	A	426	48.438	-11.054	44.030	1.00	24.91
2358	NE2	GLN	A	420	63.849	-20.928	50.243	1.00	43.71	2403	CB	THR	A	426	50.462	-11.587	42.625	1.00	24.59
2359	N	GLY	A	421	61.326	-16.936	53.690	1.00	29.02	2404	OG1	THR	A	426	50.660	-12.926	43.104	1.00	26.94
2360	CA	GLY	A	421	59.929	-16.790	54.080	1.00	27.43	2405	CG2	THR	A	426	51.843	-11.146	42.152	1.00	25.00
2361	C	GLY	A	421	59.223	-15.673	53.308	1.00	28.32	2406	N	PRO	A	427	47.481	-10.229	43.662	1.00	24.58
2362	O	GLY	A	421	58.048	-15.418	53.556	1.00	24.66	2407	CA	PRO	A	427	46.078	-10.493	43.995	1.00	22.44
2363	N	ASP	A	422	59.878	-15.004	52.358	1.00	28.80	2408	C	PRO	A	427	45.481	-11.448	42.987	1.00	19.97
2364	CA	ASP	A	422	59.295	-13.889	51.627	1.00	30.89	2409	O	PRO	A	427	46.143	-11.846	42.015	1.00	18.98
2365	C	ASP	A	422	58.088	-14.200	50.738	1.00	36.19	2410	CB	PRO	A	427	45.449	-9.098	43.970	1.00	22.44
2366	O	ASP	A	422	58.230	-14.870	49.727	1.00	38.46	2411	CG	PRO	A	427	46.215	-8.410	42.886	1.00	23.34
2367	CB	ASP	A	422	60.420	-13.227	50.804	1.00	27.10	2412	CD	PRO	A	427	47.643	-8.943	42.956	1.00	24.22
2368	CG	ASP	A	422	59.951	-11.980	50.032	1.00	25.30	2413	N	ALA	A	428	44.221	-11.818	43.186	1.00	18.32
2369	OD1	ASP	A	422	59.222	-11.152	50.594	1.00	23.55	2414	CA	ALA	A	428	43.524	-12.705	42.287	1.00	18.67
2370	OD2	ASP	A	422	60.287	-11.929	48.830	1.00	22.98	2415	C	ALA	A	428	43.302	-12.115	40.901	1.00	18.57
2371	N	HIS	A	423	56.911	-13.629	51.020	1.00	40.93	2416	O	ALA	A	428	43.391	-12.950	39.990	1.00	18.53
2372	CA	HIS	A	423	55.703	-13.849	50.233	1.00	47.21	2417	CB	ALA	A	428	42.176	-13.179	42.853	1.00	19.42
2373	C	HIS	A	423	55.313	-12.763	49.209	1.00	45.37	2418	N	ASN	A	429	43.248	-10.788	40.730	1.00	16.60
2374	O	HIS	A	423	54.768	-11.681	49.406	1.00	47.07	2419	CA	ASN	A	429	43.080	-10.263	39.358	1.00	15.96
2375	CB	HIS	A	423	54.512	-14.100	51.176	1.00	51.41	2420	C	ASN	A	429	43.673	-8.877	39.366	1.00	16.94
2376	CG	HIS	A	423	53.238	-14.617	50.601	1.00	56.21	2421	O	ASN	A	429	43.676	-8.221	40.413	1.00	17.66
2377	ND1	HIS	A	423	52.275	-13.795	50.033	1.00	58.05	2422	CB	ASN	A	429	41.572	-10.199	39.015	1.00	15.37
2378	CD2	HIS	A	423	52.745	-15.896	50.562	1.00	57.47	2423	CG	ASN	A	429	41.218	-9.874	37.587	1.00	14.52
2379	CE1	HIS	A	423	51.265	-14.568	49.639	1.00	58.60	2424	OD1	ASN	A	429	40.864	-10.725	36.749	1.00	17.02
2380	NE2	HIS	A	423	51.519	-15.838	49.939	1.00	58.38	2425	ND2	ASN	A	429	41.224	-8.619	37.164	1.00	12.11

4496	C	ASP A 693	48.252	21.124	25.925	1.00	20.25	4541	CG	PHE A 699	34.419	14.751	32.963	1.00	18.86
4497	O	ASP A 693	47.300	20.850	26.671	1.00	15.97	4542	CD1	PHE A 699	34.594	14.201	34.229	1.00	17.66
4498	CB	ASP A 693	46.932	20.849	23.734	1.00	20.28	4543	CD2	PHE A 699	33.124	14.931	32.494	1.00	17.36
4499	CG	ASP A 693	46.336	22.240	23.779	1.00	22.51	4544	CE1	PHE A 699	33.481	13.856	35.006	1.00	18.49
4500	OD1	ASP A 693	45.186	22.441	23.333	1.00	24.25	4545	CE2	PHE A 699	32.021	14.589	33.261	1.00	19.78
4501	OD2	ASP A 693	47.013	23.154	24.306	1.00	23.36	4546	CZ	PHE A 699	32.189	14.044	34.525	1.00	19.39
4502	N	LYS A 694	49.301	21.803	26.426	1.00	22.37	4547	N	ALA A 700	37.233	16.927	34.136	1.00	16.55
4503	CA	LYS A 694	49.397	22.197	27.836	1.00	26.78	4548	CA	ALA A 700	37.167	17.425	35.495	1.00	16.01
4504	C	LYS A 694	48.227	23.020	28.342	1.00	25.75	4549	C	ALA A 700	37.613	18.922	35.560	1.00	17.98
4505	O	LYS A 694	47.839	22.882	29.508	1.00	26.28	4550	O	ALA A 700	37.438	19.479	36.654	1.00	16.39
4506	CB	LYS A 694	50.739	22.873	28.133	1.00	30.68	4551	CB	ALA A 700	38.547	16.728	36.197	1.00	15.97
4507	CG	LYS A 694	50.740	24.392	28.225	1.00	35.67	4552	N	THR A 701	38.066	19.547	34.474	1.00	17.35
4508	CD	LYS A 694	52.036	24.960	28.789	1.00	39.09	4553	CA	THR A 701	38.531	20.920	34.525	1.00	18.55
4509	CE	LYS A 694	52.086	26.494	28.763	1.00	41.48	4554	C	THR A 701	37.744	21.889	33.629	1.00	19.85
4510	NZ	LYS A 694	50.861	27.195	29.329	1.00	43.73	4555	O	THR A 701	38.226	23.004	33.458	1.00	20.14
4511	N	THR A 695	47.560	23.824	27.511	1.00	23.27	4556	CB	THR A 701	40.027	21.044	34.148	1.00	18.45
4512	CA	THR A 695	46.427	24.609	27.898	1.00	24.00	4557	OG1	THR A 701	40.289	20.404	32.895	1.00	18.96
4513	C	THR A 695	45.076	23.936	27.789	1.00	21.80	4558	CG2	THR A 701	40.941	20.438	35.213	1.00	19.17
4514	O	THR A 695	44.094	24.597	28.158	1.00	23.18	4559	N	GLY A 702	36.558	21.526	33.166	1.00	21.54
4515	CB	THR A 695	46.289	25.932	27.057	1.00	26.17	4560	CA	GLY A 702	35.692	22.478	32.466	1.00	23.96
4516	OG1	THR A 695	45.835	25.571	25.738	1.00	30.11	4561	C	GLY A 702	35.279	22.206	31.039	1.00	24.73
4517	CG2	THR A 695	47.536	26.727	27.038	1.00	26.32	4562	O	GLY A 702	34.407	22.929	30.527	1.00	23.67
4518	N	ALA A 696	44.970	22.725	27.246	1.00	17.97	4563	N	ASP A 703	35.873	21.237	30.342	1.00	23.12
4519	CA	ALA A 696	43.659	22.141	27.079	1.00	19.04	4564	CA	ASP A 703	35.398	20.922	28.991	1.00	23.82
4520	C	ALA A 696	43.034	21.799	28.438	1.00	18.20	4565	C	ASP A 703	34.070	20.187	29.093	1.00	23.19
4521	O	ALA A 696	43.750	21.502	29.404	1.00	17.08	4566	O	ASP A 703	33.960	19.175	29.779	1.00	18.58
4522	CB	ALA A 696	43.747	20.900	26.195	1.00	18.12	4567	CB	ASP A 703	36.431	20.071	28.241	1.00	23.36
4523	N	GLN A 697	41.724	21.764	28.480	1.00	17.77	4568	CG	ASP A 703	36.033	19.782	26.797	1.00	24.04
4524	CA	GLN A 697	40.935	21.340	29.647	1.00	18.85	4569	OD1	ASP A 703	36.618	20.476	25.930	1.00	25.71
4525	C	GLN A 697	40.214	20.039	29.320	1.00	19.35	4570	OD2	ASP A 703	35.168	18.926	26.500	1.00	21.20
4526	O	GLN A 697	40.134	19.653	28.146	1.00	18.13	4571	N	PRO A 704	33.059	20.609	28.324	1.00	24.11
4527	CB	GLN A 697	39.886	22.400	30.046	1.00	21.26	4572	CA	PRO A 704	31.731	20.018	28.400	1.00	23.04
4528	CG	GLN A 697	40.464	23.763	30.408	1.00	21.40	4573	C	PRO A 704	31.480	18.888	27.446	1.00	21.55
4529	CD	GLN A 697	39.454	24.837	30.803	1.00	23.53	4574	O	PRO A 704	30.401	18.265	27.492	1.00	21.23
4530	OE1	GLN A 697	39.895	25.823	31.487	1.00	25.32	4575	CB	PRO A 704	30.809	21.220	28.065	1.00	24.82
4531	NE2	GLN A 697	38.206	24.668	30.518	1.00	20.87	4576	CG	PRO A 704	31.633	21.977	27.058	1.00	25.35
4532	N	GLY A 698	39.716	19.300	30.312	1.00	18.21	4577	CD	PRO A 704	33.080	21.823	27.468	1.00	24.45
4533	CA	GLY A 698	38.991	18.051	30.069	1.00	16.88	4578	N	ASN A 705	32.447	18.525	26.606	1.00	19.72
4534	C	GLY A 698	37.739	17.973	30.988	1.00	18.11	4579	CA	ASN A 705	32.185	17.446	25.629	1.00	21.46
4535	O	GLY A 698	37.289	19.027	31.463	1.00	18.21	4580	C	ASN A 705	32.884	15.294	24.976	1.00	23.47
4536	N	PHE A 699	37.184	16.788	31.222	1.00	16.37	4581	O	ASN A 705	32.802	16.090	25.927	1.00	23.27
4537	CA	PHE A 699	35.989	16.611	32.032	1.00	18.23	4582	CB	ASN A 705	32.745	17.969	24.290	1.00	21.14
4538	C	PHE A 699	36.113	17.182	33.445	1.00	18.02	4583	CG	ASN A 705	32.042	19.276	23.915	1.00	23.28
4539	O	PHE A 699	35.197	17.064	33.906	1.00	16.59	4584	OD1	ASN A 705	30.818	19.366	24.062	1.00	23.01
4540	CB	PHE A 699	35.608	15.121	32.107	1.00	17.98	4585	ND2	ASN A 705	32.790	20.256	23.491	1.00	24.52

4766	CB	ASN A 730	41.764	3.781	34.807	1.00	16.99	4811	NE2	HIS A 735	58.586	8.039	32.480	1.00	16.01
4767	CG	ASN A 730	40.776	2.775	34.203	1.00	16.76	4812	N	ASP A 736	56.069	11.050	32.912	1.00	18.06
4768	OD1	ASN A 730	39.932	2.076	34.846	1.00	17.80	4813	CA	ASP A 736	56.221	11.847	31.698	1.00	18.55
4769	ND2	ASN A 730	40.923	2.747	32.900	1.00	14.18	4814	C	ASP A 736	55.296	13.073	31.785	1.00	19.59
4770	N	TYR A 731	44.303	6.022	34.261	1.00	14.78	4815	O	ASP A 736	54.252	13.058	32.472	1.00	14.38
4771	CA	TYR A 731	45.135	7.013	34.912	1.00	16.43	4816	CB	ASP A 736	55.851	11.014	30.458	1.00	19.05
4772	C	TYR A 731	44.889	8.442	34.401	1.00	16.43	4817	CG	ASP A 736	56.916	10.045	29.971	1.00	19.36
4773	O	TYR A 731	44.321	8.554	33.309	1.00	16.09	4818	OD1	ASP A 736	58.079	10.474	29.782	1.00	18.46
4774	CB	TYR A 731	46.641	6.738	34.752	1.00	16.77	4819	OD2	ASP A 736	56.639	8.828	29.769	1.00	19.23
4775	CG	TYR A 731	47.189	6.951	33.358	1.00	17.72	4820	N	ASN A 737	55.648	14.149	31.055	1.00	19.40
4776	CD1	TYR A 731	48.208	7.865	33.101	1.00	18.91	4821	CA	ASN A 737	54.827	15.353	31.031	1.00	19.79
4777	CD2	TYR A 731	46.723	6.190	32.306	1.00	16.97	4822	C	ASN A 737	54.651	15.987	32.411	1.00	20.31
4778	CE1	TYR A 731	48.689	8.074	31.810	1.00	20.50	4823	O	ASN A 737	55.545	15.914	33.270	1.00	18.64
4779	CE2	TYR A 731	47.152	6.393	31.015	1.00	19.21	4824	CB	ASN A 737	53.499	15.028	30.295	1.00	20.11
4780	CZ	TYR A 731	48.157	7.321	30.782	1.00	22.10	4825	CG	ASN A 737	53.794	14.336	28.972	1.00	23.21
4781	OH	TYR A 731	48.585	7.473	29.473	1.00	22.66	4826	OD1	ASN A 737	53.500	13.160	28.760	1.00	23.28
4782	N	VAL A 732	45.463	9.396	35.150	1.00	14.45	4827	ND2	ASN A 737	54.473	14.985	28.022	1.00	23.64
4783	CA	VAL A 732	45.429	10.782	34.652	1.00	15.94	4828	N	MET A 738	53.530	16.651	32.711	1.00	19.26
4784	C	VAL A 732	46.793	11.401	34.486	1.00	15.92	4829	CA	MET A 738	53.389	17.416	33.938	1.00	19.59
4785	O	VAL A 732	46.949	12.340	33.663	1.00	16.20	4830	O	MET A 738	51.854	15.813	34.846	1.00	17.92
4786	CB	VAL A 732	44.507	11.667	35.541	1.00	16.99	4831	C	MET A 738	52.619	18.711	33.619	1.00	20.83
4787	CG1	VAL A 732	44.997	11.697	36.988	1.00	13.37	4832	CB	MET A 738	53.300	19.598	32.561	1.00	22.68
4788	CG2	VAL A 732	44.444	13.123	35.006	1.00	17.23	4833	CG	MET A 738	52.260	21.070	32.188	1.00	25.13
4789	N	THR A 733	47.822	11.034	35.242	1.00	15.69	4834	OD1	MET A 738	52.603	22.154	33.456	1.00	22.07
4790	CA	THR A 733	49.189	11.535	35.142	1.00	16.13	4835	CE	MET A 738	52.939	17.124	36.311	1.00	17.76
4791	C	THR A 733	50.244	10.428	35.359	1.00	16.11	4836	N	THR A 739	52.155	16.614	37.447	1.00	18.00
4792	O	THR A 733	49.918	9.357	35.898	1.00	13.88	4837	CA	THR A 739	50.770	17.275	37.332	1.00	18.02
4793	CB	THR A 733	49.597	12.657	36.115	1.00	17.42	4838	C	THR A 739	50.609	18.312	36.672	1.00	18.06
4794	OG1	THR A 733	49.438	12.231	37.477	1.00	15.92	4839	O	THR A 739	52.781	16.952	38.809	1.00	19.29
4795	CG2	THR A 733	48.827	13.958	35.888	1.00	14.57	4840	CB	THR A 739	52.642	18.358	39.103	1.00	17.62
4796	N	SER A 734	51.504	10.693	34.974	1.00	16.76	4841	OG1	THR A 739	54.267	16.607	38.889	1.00	17.97
4797	CA	SER A 734	52.607	9.753	35.168	1.00	16.69	4842	CG2	THR A 739	49.739	16.694	37.916	1.00	16.11
4798	C	SER A 734	53.925	10.520	35.190	1.00	17.73	4843	N	LEU A 740	48.403	17.232	37.843	1.00	17.22
4799	O	SER A 734	53.869	11.751	35.123	1.00	18.37	4844	CA	LEU A 740	48.315	18.636	38.430	1.00	16.52
4800	CB	SER A 734	52.699	8.630	34.116	1.00	16.19	4845	C	LEU A 740	47.642	19.447	37.769	1.00	17.44
4801	OG	SER A 734	53.031	9.220	32.839	1.00	17.55	4846	O	LEU A 740	47.300	16.323	38.417	1.00	15.94
4802	N	HIS A 735	55.095	9.901	35.332	1.00	16.87	4847	CB	LEU A 740	45.862	16.743	38.020	1.00	16.72
4803	CA	HIS A 735	56.355	10.627	35.335	1.00	18.13	4848	C	LEU A 740	45.757	16.769	36.484	1.00	16.81
4804	C	HIS A 735	56.582	11.454	34.067	1.00	18.58	4849	CD1	LEU A 740	44.836	15.720	38.527	1.00	14.02
4805	O	HIS A 735	57.307	12.484	34.165	1.00	20.77	4850	CD2	LEU A 740	48.917	18.934	39.557	1.00	16.04
4806	CB	HIS A 735	57.585	9.714	35.570	1.00	16.15	4851	N	TRP A 741	48.920	20.276	40.119	1.00	18.09
4807	CG	HIS A 735	57.897	8.867	34.358	1.00	16.14	4852	CA	TRP A 741	48.917	18.934	39.557	1.00	16.04
4808	ND1	HIS A 735	57.309	7.621	34.171	1.00	13.70	4853	C	TRP A 741	49.452	21.316	39.117	1.00	20.12
4809	CD2	HIS A 735	58.707	9.141	33.286	1.00	14.91	4854	O	TRP A 741	48.838	22.376	38.903	1.00	20.13
4810	CE1	HIS A 735	57.772	7.135	33.010	1.00	16.16	4855	CR	TRP A 741	49.692	20.303	41.435	1.00	17.80

5036	O	HIS A 764	40.318	8.959	41.071	1.00 14.64	5081	CA	SER A 770	35.921	3.261	37.631	1.00 14.16
5037	CB	HIS A 764	42.523	11.373	41.764	1.00 16.48	5082	C	SER A 770	36.302	1.788	37.682	1.00 14.69
5038	CG	HIS A 764	43.881	11.820	41.290	1.00 16.16	5083	O	SER A 770	37.326	1.408	38.247	1.00 13.64
5039	ND1	HIS A 764	44.861	10.897	40.931	1.00 17.78	5084	CB	SER A 770	36.746	3.878	36.481	1.00 14.15
5040	CD2	HIS A 764	44.425	13.045	41.106	1.00 14.29	5085	OG	SER A 770	36.278	5.140	36.080	1.00 11.77
5041	CE1	HIS A 764	45.980	11.539	40.576	1.00 13.10	5086	N	GLN A 771	35.626	0.960	36.880	1.00 13.77
5042	NE2	HIS A 764	45.734	12.822	40.663	1.00 18.06	5087	CA	GLN A 771	36.006	-0.422	36.664	1.00 13.99
5043	N	ALA A 765	39.263	10.853	41.598	1.00 14.85	5088	C	GLN A 771	37.356	-0.464	35.925	1.00 15.46
5044	CA	ALA A 765	38.050	10.167	42.039	1.00 15.19	5089	O	GLN A 771	37.647	0.442	35.136	1.00 12.49
5045	C	ALA A 765	37.481	9.281	40.923	1.00 15.79	5090	CB	GLN A 771	34.970	-1.223	35.849	1.00 13.53
5046	O	ALA A 765	36.976	8.170	41.144	1.00 15.86	5091	CG	GLN A 771	33.544	-1.161	36.443	1.00 13.08
5047	CB	ALA A 765	36.973	11.185	42.490	1.00 15.09	5092	CD	GLN A 771	33.426	-1.789	37.822	1.00 14.69
5048	N	VAL A 766	37.426	9.768	39.691	1.00 15.11	5093	OB1	GLN A 771	32.830	-1.185	38.752	1.00 17.76
5049	CA	VAL A 766	37.011	8.984	38.524	1.00 14.49	5094	NE2	GLN A 771	33.956	-2.976	38.040	1.00 10.21
5051	O	VAL A 766	37.969	7.801	38.348	1.00 15.68	5095	N	GLY A 772	38.232	-1.456	36.210	1.00 15.16
5052	CB	VAL A 766	37.484	6.669	38.206	1.00 15.59	5096	CA	GLY A 772	39.559	-1.446	35.598	1.00 14.97
5053	CG1	VAL A 766	36.639	9.813	37.215	1.00 14.83	5097	C	GLY A 772	40.698	-1.432	36.635	1.00 17.39
5054	CG2	VAL A 766	35.898	10.921	37.371	1.00 13.49	5098	O	GLY A 772	40.444	-1.663	37.829	1.00 17.47
5055	N	VAL A 767	39.295	8.026	38.448	1.00 15.32	5099	N	VAL A 773	41.944	-1.109	36.210	1.00 14.33
5056	CA	VAL A 767	40.182	6.831	38.337	1.00 15.78	5100	CA	VAL A 773	43.079	-1.067	37.150	1.00 14.45
5057	C	VAL A 767	39.874	5.778	39.405	1.00 16.72	5101	C	VAL A 773	43.498	0.376	37.463	1.00 14.94
5058	O	VAL A 767	39.783	4.553	39.099	1.00 16.35	5102	O	VAL A 773	44.084	0.998	36.611	1.00 16.35
5059	CB	VAL A 767	41.656	7.260	38.475	1.00 15.24	5103	CB1	VAL A 773	44.310	-1.795	36.560	1.00 13.88
5060	CG1	VAL A 767	42.610	6.067	38.588	1.00 13.41	5104	CG2	VAL A 773	45.422	-1.889	37.632	1.00 14.66
5061	CG2	VAL A 767	42.126	8.151	37.317	1.00 14.80	5105	N	PRO A 774	44.005	-3.217	36.086	1.00 12.67
5062	N	PHE A 768	39.717	6.221	40.658	1.00 16.27	5106	C	PRO A 774	43.257	0.966	38.599	1.00 13.58
5063	CA	PHE A 768	39.471	5.305	41.772	1.00 16.07	5107	CA	PRO A 774	45.167	2.545	39.130	1.00 15.75
5064	C	PHE A 768	38.094	4.659	41.812	1.00 16.53	5108	C	PRO A 774	45.813	1.748	39.817	1.00 15.14
5065	O	PHE A 768	37.996	3.555	42.413	1.00 15.90	5109	O	PRO A 774	42.834	2.611	40.199	1.00 14.18
5066	CB	PHE A 768	39.838	5.868	43.137	1.00 15.94	5110	CB	PRO A 774	42.710	1.231	40.899	1.00 14.41
5067	CG	PHE A 768	41.238	6.460	43.307	1.00 16.54	5111	CG	PRO A 774	42.527	0.274	39.729	1.00 13.83
5068	CD1	PHE A 768	41.402	7.676	43.923	1.00 15.00	5112	CD	PRO A 774	45.788	3.610	38.635	1.00 14.44
5069	CD2	PHE A 768	42.374	5.808	42.882	1.00 17.09	5113	N	PHE A 775	47.223	3.894	38.687	1.00 13.52
5070	CE1	PHE A 768	42.654	8.258	44.120	1.00 16.04	5114	CA	PHE A 775	47.368	5.379	39.009	1.00 15.10
5071	CE2	PHE A 768	43.640	6.366	43.042	1.00 17.04	5115	C	PHE A 775	46.501	6.130	38.554	1.00 13.30
5072	CZ	PHE A 768	43.783	7.583	43.673	1.00 16.63	5116	O	PHE A 775	47.900	3.601	37.345	1.00 12.64
5073	N	THR A 769	37.041	5.156	41.149	1.00 15.47	5117	CB	PHE A 775	49.278	4.170	37.094	1.00 13.05
5074	CA	THR A 769	35.736	4.475	41.230	1.00 14.36	5118	CG	PHE A 775	49.496	5.505	36.842	1.00 12.94
5075	C	THR A 769	35.328	3.823	39.920	1.00 15.61	5119	CD1	PHE A 775	50.356	3.300	37.074	1.00 14.88
5076	O	THR A 769	34.198	3.269	39.801	1.00 15.87	5120	CE1	PHE A 775	50.749	6.040	36.616	1.00 15.54
5077	CB	THR A 769	34.620	5.443	41.691	1.00 15.41	5121	CE2	PHE A 775	51.633	3.813	36.809	1.00 16.38
5078	OG1	THR A 769	34.713	6.617	40.902	1.00 14.96	5122	CZ	PHE A 775	51.828	5.157	36.592	1.00 15.45
5079	CG2	THR A 769	34.762	5.855	43.174	1.00 15.33	5123	N	MET A 776	48.332	5.763	39.836	1.00 14.40
5080	N	SER A 770	36.220	3.901	38.906	1.00 14.01	5124	CA	MET A 776	48.537	7.192	40.097	1.00 15.32

5126	C	MET A 776	50.042	7.492	40.068	1.00	16.66	5171	CB	MET A 782	51.460	15.657	49.216	1.00	19.24
5127	O	MET A 776	50.796	6.561	40.340	1.00	16.26	5172	CG	MET A 782	52.667	14.956	48.626	1.00	21.00
5128	CB	MET A 776	47.999	7.642	41.453	1.00	14.34	5173	SD	MET A 782	53.939	14.548	49.843	1.00	19.47
5129	CG	MET A 776	48.432	6.833	42.653	1.00	15.93	5174	CE	MET A 782	55.206	13.871	48.770	1.00	24.22
5130	SD	MET A 776	47.677	7.342	44.233	1.00	13.48	5175	N	LEU A 783	49.947	17.109	46.165	1.00	17.38
5131	CE	MET A 776	48.304	9.017	44.325	1.00	14.69	5176	CA	LEU A 783	50.155	18.163	45.193	1.00	18.72
5132	N	GLN A 777	50.420	8.732	39.804	1.00	16.06	5177	C	LEU A 783	51.620	18.346	44.767	1.00	19.18
5133	CA	GLN A 777	51.838	9.108	39.931	1.00	15.06	5178	O	LEU A 783	52.145	19.459	44.641	1.00	18.25
5134	C	GLN A 777	52.082	9.345	41.420	1.00	13.74	5179	CB	LEU A 783	49.475	19.451	45.699	1.00	17.56
5135	O	GLN A 777	51.281	10.097	41.996	1.00	12.00	5180	CG	LEU A 783	48.014	19.300	46.199	1.00	17.76
5136	CB	GLN A 777	52.175	10.388	39.136	1.00	15.88	5181	CD1	LEU A 783	47.488	20.670	46.671	1.00	17.88
5137	CG	GLN A 777	53.660	10.809	39.318	1.00	14.21	5182	CD2	LEU A 783	47.044	18.790	45.147	1.00	17.03
5138	CD	GLN A 777	54.081	12.028	38.491	1.00	16.72	5183	N	ARG A 784	52.365	17.273	44.548	1.00	18.59
5139	OE1	GLN A 777	55.294	12.354	38.396	1.00	15.28	5184	CA	ARG A 784	53.781	17.338	44.128	1.00	16.30
5140	NE2	GLN A 777	53.132	12.777	37.931	1.00	13.34	5185	C	ARG A 784	53.899	18.310	42.947	1.00	16.06
5141	N	GLY A 778	53.109	8.770	42.037	1.00	14.51	5186	O	ARG A 784	53.105	18.204	42.016	1.00	13.00
5142	CA	GLY A 778	53.354	8.968	43.469	1.00	12.51	5187	CB	ARG A 784	54.303	15.965	43.754	1.00	16.36
5143	C	GLY A 778	53.552	10.434	43.782	1.00	15.81	5188	CG	ARG A 784	55.732	15.917	43.128	1.00	15.05
5144	O	GLY A 778	54.236	11.120	42.976	1.00	16.75	5189	CD	ARG A 784	56.414	14.612	43.471	1.00	14.37
5145	N	GLY A 779	52.939	10.912	44.890	1.00	14.20	5190	NE	ARG A 784	57.508	14.212	42.581	1.00	15.11
5146	CA	GLY A 779	53.108	12.345	45.197	1.00	14.32	5191	CZ	ARG A 784	57.463	13.745	41.344	1.00	15.39
5147	C	GLY A 779	51.919	13.204	44.778	1.00	13.35	5192	NH1	ARG A 784	56.328	13.510	40.649	1.00	14.22
5148	O	GLY A 779	51.774	14.341	45.263	1.00	13.40	5193	NH2	ARG A 784	58.620	13.430	40.733	1.00	14.18
5149	N	GLU A 780	51.027	12.713	43.910	1.00	12.45	5194	CA	THR A 785	54.889	19.199	42.961	1.00	16.44
5150	CA	GLU A 780	49.829	13.482	43.533	1.00	12.05	5195	CA	THR A 785	55.115	20.158	41.892	1.00	15.86
5151	C	GLU A 780	48.913	13.718	44.746	1.00	14.09	5196	C	THR A 785	56.506	20.037	41.278	1.00	17.13
5152	O	GLU A 780	48.336	14.808	44.855	1.00	15.37	5197	O	THR A 785	57.501	19.843	41.965	1.00	17.03
5153	CB	GLU A 780	48.989	12.898	42.410	1.00	13.91	5198	CB	THR A 785	54.867	21.626	42.325	1.00	16.69
5154	CG	GLU A 780	49.577	12.770	41.025	1.00	16.76	5199	OG1	THR A 785	55.174	22.534	41.239	1.00	15.16
5155	CD	GLU A 780	50.238	13.981	40.396	1.00	20.75	5200	CG2	THR A 785	55.649	22.074	43.552	1.00	17.25
5156	OE1	GLU A 780	51.146	14.633	41.024	1.00	19.70	5201	N	LYS A 786	56.614	20.188	39.958	1.00	18.17
5157	OE2	GLU A 780	49.891	14.243	39.214	1.00	19.72	5202	CA	LYS A 786	57.921	20.173	39.294	1.00	17.98
5158	N	GLU A 781	48.866	12.843	45.725	1.00	14.52	5203	C	LYS A 786	59.229	21.610	38.838	1.00	19.45
5159	CA	GLU A 781	48.154	12.941	46.974	1.00	15.90	5204	O	LYS A 786	57.921	20.173	39.294	1.00	17.98
5160	C	GLU A 781	48.654	14.108	47.829	1.00	18.04	5205	CB	LYS A 786	59.132	21.831	38.027	1.00	18.14
5161	O	GLU A 781	47.923	14.505	48.739	1.00	16.36	5206	CG	LYS A 786	57.954	17.750	38.423	1.00	14.96
5162	CB	GLU A 781	48.261	11.644	47.797	1.00	15.13	5207	CD	LYS A 786	57.859	16.802	37.187	1.00	14.97
5163	CG	GLU A 781	49.627	11.402	48.399	1.00	16.08	5208	CE	LYS A 786	57.877	15.352	37.713	1.00	15.19
5164	CD	GLU A 781	50.695	10.808	47.504	1.00	16.18	5209	NZ	LYS A 786	57.719	14.341	36.641	1.00	16.24
5165	OE1	GLU A 781	51.749	10.429	48.068	1.00	16.29	5210	N	GLY A 787	57.436	22.583	39.295	1.00	18.49
5166	OE2	GLU A 781	50.534	10.719	46.283	1.00	13.64	5211	CA	GLY A 787	57.644	23.974	38.910	1.00	20.70
5167	N	MET A 782	49.842	14.681	47.552	1.00	18.10	5212	C	GLY A 787	57.258	24.206	37.454	1.00	22.88
5168	CA	MET A 782	50.278	15.860	48.278	1.00	18.57	5213	O	GLY A 787	57.860	25.094	36.818	1.00	23.87
5169	C	MET A 782	50.588	17.012	47.311	1.00	18.29	5214	N	GLY A 788	56.399	23.347	36.861	1.00	21.35
5170	O	MET A 782	51.393	17.853	47.652	1.00	19.99	5215	CA	GLY A 788	56.109	23.489	35.452	1.00	21.36

5306	N	GLN A 801	61.969	15.783	43.590	1.00	14.69	5351	O	SER A 805	54.135	20.065	53.884	1.00	23.61
5307	CA	GLN A 801	61.866	15.102	44.861	1.00	18.63	5352	CB	SER A 805	57.197	20.695	53.829	1.00	19.87
5308	C	GLN A 801	60.471	15.071	45.487	1.00	16.56	5353	OG	SER A 805	57.187	21.301	52.527	1.00	19.02
5309	O	GLN A 801	59.644	15.874	45.101	1.00	15.25	5354	N	ARG A 806	54.822	19.172	51.974	1.00	19.88
5310	CB	GLN A 801	62.806	15.707	45.932	1.00	17.66	5355	CA	ARG A 806	53.512	19.335	51.351	1.00	22.24
5311	CG	GLN A 801	62.342	17.090	46.382	1.00	19.69	5356	C	ARG A 806	52.442	18.396	51.883	1.00	21.51
5312	CD	GLN A 801	63.483	17.927	46.966	1.00	21.59	5357	O	ARG A 806	51.254	18.722	51.750	1.00	19.94
5313	OE1	GLN A 801	64.500	17.414	47.435	1.00	22.85	5358	CB	ARG A 806	53.636	19.156	49.822	1.00	24.11
5314	NE2	GLN A 801	63.304	19.240	47.068	1.00	21.07	5359	CG	ARG A 806	54.034	20.543	49.260	1.00	26.24
5315	N	PHE A 802	60.305	14.158	46.429	1.00	16.13	5360	CD	ARG A 806	54.401	20.399	47.801	1.00	24.25
5316	CA	PHE A 802	59.071	14.118	47.240	1.00	18.13	5361	NE	ARG A 806	53.327	20.788	46.893	1.00	21.27
5317	C	PHE A 802	59.323	15.192	48.327	1.00	18.45	5362	CZ	ARG A 806	53.057	22.032	46.574	1.00	20.40
5318	O	PHE A 802	60.112	14.942	49.246	1.00	19.38	5363	NH1	ARG A 806	53.779	23.031	47.094	1.00	21.72
5319	CB	PHE A 802	58.763	12.759	47.875	1.00	16.57	5364	NH2	ARG A 806	52.132	22.253	45.677	1.00	18.36
5320	CG	PHE A 802	58.053	11.737	47.006	1.00	19.68	5365	N	LYS A 807	52.841	17.251	52.437	1.00	20.38
5321	CD1	PHE A 802	58.287	11.656	45.645	1.00	18.62	5366	CA	LYS A 807	51.865	16.365	53.068	1.00	20.37
5322	CD2	PHE A 802	57.109	10.859	47.565	1.00	20.70	5367	C	LYS A 807	51.298	17.082	54.296	1.00	21.65
5323	CE1	PHE A 802	57.590	10.747	44.860	1.00	20.67	5368	O	LYS A 807	50.107	17.019	54.552	1.00	21.63
5324	CE2	PHE A 802	56.413	9.938	46.778	1.00	20.96	5369	CB	LYS A 807	52.501	15.007	53.414	1.00	17.10
5325	CZ	PHE A 802	56.693	9.865	45.429	1.00	19.43	5370	CG	LYS A 807	51.504	14.093	54.081	1.00	18.69
5326	N	ASP A 803	58.624	16.288	48.253	1.00	18.57	5371	CD	LYS A 807	52.030	12.677	54.344	1.00	16.56
5327	CA	ASP A 803	58.808	17.357	49.254	1.00	19.86	5372	CE	LYS A 807	50.960	11.883	55.134	1.00	15.71
5328	C	ASP A 803	57.793	17.081	50.357	1.00	20.28	5373	NZ	LYS A 807	51.497	10.512	55.378	1.00	14.68
5329	O	ASP A 803	56.641	17.492	50.205	1.00	19.15	5374	N	ALA A 808	52.112	17.787	55.077	1.00	20.44
5330	CB	ASP A 803	58.610	18.731	48.651	1.00	22.65	5375	CA	ALA A 808	51.606	18.577	56.202	1.00	23.20
5331	CG	ASP A 803	58.669	19.930	49.590	1.00	25.08	5376	C	ALA A 808	50.732	19.752	55.729	1.00	22.93
5332	OD1	ASP A 803	58.806	19.685	50.814	1.00	23.70	5377	O	ALA A 808	49.629	19.995	56.232	1.00	22.27
5333	OD2	ASP A 803	58.588	21.104	49.167	1.00	25.27	5378	CB	ALA A 808	52.751	19.163	57.024	1.00	21.77
5334	N	TRP A 804	58.233	16.380	51.405	1.00	18.05	5379	N	GLN A 809	51.188	20.477	54.706	1.00	23.92
5335	CA	TRP A 804	57.319	15.921	52.445	1.00	19.41	5380	CA	GLN A 809	50.492	21.617	54.146	1.00	23.89
5336	C	TRP A 804	56.629	16.989	53.289	1.00	21.10	5381	C	GLN A 809	49.162	21.215	53.507	1.00	23.43
5337	O	TRP A 804	55.653	16.669	53.993	1.00	19.44	5382	O	GLN A 809	48.168	21.944	53.608	1.00	20.37
5338	CB	TRP A 804	57.946	14.789	53.243	1.00	18.06	5383	CB	GLN A 809	51.356	22.355	53.095	1.00	25.14
5339	CG	TRP A 804	58.290	13.537	52.497	1.00	19.31	5384	CG	GLN A 809	50.627	23.521	52.421	1.00	26.75
5340	CD1	TRP A 804	59.477	13.263	51.863	1.00	18.88	5385	CD	GLN A 809	51.547	24.361	51.551	1.00	29.36
5341	CD2	TRP A 804	57.474	12.380	52.297	1.00	19.81	5386	OE1	GLN A 809	52.735	24.031	51.422	1.00	28.08
5342	NE1	TRP A 804	59.448	12.034	51.283	1.00	18.40	5387	NE2	GLN A 809	51.050	25.449	50.941	1.00	30.28
5343	CE2	TRP A 804	58.216	11.461	51.531	1.00	18.59	5388	N	PHE A 810	49.159	20.078	52.774	1.00	22.26
5344	CE3	TRP A 804	56.163	12.061	52.677	1.00	18.95	5389	CA	PHE A 810	47.883	19.685	52.166	1.00	21.21
5345	CZ2	TRP A 804	57.722	10.222	51.155	1.00	17.95	5390	C	PHE A 810	47.375	18.387	52.769	1.00	21.19
5346	CZ3	TRP A 804	55.674	10.809	52.304	1.00	18.76	5391	O	PHE A 810	46.913	17.517	52.055	1.00	20.62
5347	CH2	TRP A 804	56.437	9.922	51.551	1.00	17.47	5392	CB	PHE A 810	47.972	19.699	50.628	1.00	21.55
5348	N	SER A 805	57.047	18.260	53.210	1.00	21.38	5393	CG	PHE A 810	48.291	21.048	50.004	1.00	21.38
5349	CA	SER A 805	56.412	19.375	53.886	1.00	21.85	5394	CD1	PHE A 810	49.557	21.281	49.481	1.00	20.93
5350	C	SER A 805	55.047	19.592	53.219	1.00	21.71	5395	CD2	PHE A 810	47.348	22.067	49.928	1.00	21.54

5396	CE1 PHE A 810	49.832	22.549	48.923	1.00	22.85	5441	OD2 ASP A 815	43.252	13.962	56.862	1.00	21.01
5397	CE2 PHE A 810	47.627	23.285	49.368	1.00	21.34	5442	N TYR A 816	41.683	12.885	51.710	1.00	16.33
5398	CZ PHE A 810	48.881	23.513	48.856	1.00	22.67	5443	CA TYR A 816	40.663	12.564	50.678	1.00	16.00
5399	N LYS A 811	47.406	18.195	54.087	1.00	21.74	5444	C TYR A 816	41.171	11.496	49.742	1.00	15.70
5400	CA LYS A 811	46.912	16.982	54.753	1.00	21.92	5445	O TYR A 816	40.397	10.580	49.417	1.00	16.79
5401	C LYS A 811	45.455	16.673	54.422	1.00	21.36	5446	CB TYR A 816	40.309	13.837	49.869	1.00	16.36
5402	O LYS A 811	45.136	15.481	54.277	1.00	17.59	5447	CG TYR A 816	39.217	13.680	48.824	1.00	15.25
5403	CB LYS A 811	47.062	17.024	56.289	1.00	23.82	5448	CD1 TYR A 816	39.444	13.129	47.564	1.00	15.93
5404	CG LYS A 811	46.896	15.669	56.992	1.00	25.05	5449	CD2 TYR A 816	37.918	14.077	49.117	1.00	15.92
5405	CD LYS A 811	47.863	14.620	56.452	1.00	27.06	5450	CE1 TYR A 816	38.400	12.970	46.633	1.00	15.05
5406	CE LYS A 811	48.035	13.364	57.285	1.00	27.83	5451	CE2 TYR A 816	36.886	13.958	48.209	1.00	16.61
5407	NZ LYS A 811	46.792	12.947	57.977	1.00	30.70	5452	CZ TYR A 816	37.111	13.358	46.984	1.00	17.64
5408	N ASP A 812	44.587	17.696	54.229	1.00	20.57	5453	OH TYR A 816	36.060	13.227	46.088	1.00	19.15
5409	CA ASP A 812	43.212	17.388	53.835	1.00	21.91	5454	N PHE A 817	42.434	11.487	49.320	1.00	12.51
5410	C ASP A 812	43.149	16.742	52.456	1.00	20.65	5455	CA PHE A 817	42.962	10.474	48.436	1.00	13.42
5411	O ASP A 812	42.273	15.900	52.246	1.00	18.27	5456	C PHE A 817	42.911	9.109	49.162	1.00	13.97
5412	CB ASP A 812	42.210	18.549	53.848	1.00	24.59	5457	O PHE A 817	42.435	8.133	48.606	1.00	13.72
5413	CG ASP A 812	42.003	19.147	55.221	1.00	28.89	5458	CB PHE A 817	44.389	10.643	47.942	1.00	13.63
5414	OD1 ASP A 812	41.473	20.283	55.328	1.00	31.55	5459	CG PHE A 817	44.578	11.514	46.713	1.00	12.99
5415	OD2 ASP A 812	42.371	18.534	56.241	1.00	28.92	5460	CD1 PHE A 817	45.189	10.988	45.577	1.00	14.35
5416	N VAL A 813	44.036	17.111	51.539	1.00	18.77	5461	CD2 PHE A 817	44.228	12.837	46.732	1.00	14.28
5417	CA VAL A 813	44.040	16.444	50.227	1.00	18.35	5462	CE1 PHE A 817	45.442	11.773	44.444	1.00	14.16
5418	C VAL A 813	44.516	15.007	50.355	1.00	16.42	5463	CE2 PHE A 817	44.474	13.644	45.615	1.00	15.25
5419	O VAL A 813	43.987	14.074	49.741	1.00	16.64	5464	CZ PHE A 817	45.056	13.124	44.486	1.00	14.04
5420	CB VAL A 813	44.922	17.275	49.264	1.00	19.35	5465	N SER A 818	43.376	9.113	50.407	1.00	12.87
5421	CG1 VAL A 813	44.998	16.618	47.885	1.00	16.35	5466	CA SER A 818	43.354	7.917	51.238	1.00	15.48
5422	CG2 VAL A 813	44.486	18.742	49.166	1.00	19.07	5467	C SER A 818	41.955	7.389	51.512	1.00	14.72
5423	N PHE A 814	45.548	14.793	51.166	1.00	16.24	5468	O SER A 818	41.744	6.162	51.485	1.00	16.73
5424	CA PHE A 814	46.057	13.444	51.406	1.00	16.82	5469	CB SER A 818	44.054	8.289	52.573	1.00	17.81
5425	C PHE A 814	44.943	12.573	51.982	1.00	17.46	5470	OG SER A 818	43.841	7.176	53.431	1.00	22.91
5426	O PHE A 814	44.795	11.422	51.542	1.00	17.98	5471	N SER A 819	40.963	8.251	51.745	1.00	15.04
5427	CB PHE A 814	47.209	13.524	52.431	1.00	16.63	5472	CA SER A 819	39.598	7.723	51.978	1.00	15.58
5428	CG PHE A 814	47.862	12.187	52.659	1.00	16.39	5473	C SER A 819	39.014	7.080	50.731	1.00	15.56
5429	CD1 PHE A 814	49.038	11.891	51.984	1.00	16.20	5474	O SER A 819	38.311	6.062	50.828	1.00	15.56
5430	CD2 PHE A 814	47.296	11.269	53.540	1.00	16.49	5475	CB SER A 819	38.630	8.852	52.401	1.00	18.73
5431	CE1 PHE A 814	49.633	10.652	52.204	1.00	17.12	5476	OG SER A 819	39.098	9.381	53.642	1.00	18.88
5432	CE2 PHE A 814	47.896	10.030	53.752	1.00	18.46	5477	N MET A 820	39.241	7.652	49.551	1.00	16.10
5433	CZ PHE A 814	49.062	9.746	53.077	1.00	18.20	5478	CA MET A 820	38.739	7.072	48.304	1.00	18.56
5434	N ASP A 815	44.207	13.085	52.974	1.00	15.05	5479	C MET A 820	39.374	5.710	48.019	1.00	18.57
5435	CA ASP A 815	43.133	12.307	53.595	1.00	17.46	5480	O MET A 820	38.727	4.747	47.598	1.00	16.01
5436	C ASP A 815	42.017	11.960	52.607	1.00	16.89	5481	CB MET A 820	39.001	8.018	47.123	1.00	20.82
5437	O ASP A 815	41.334	10.919	52.706	1.00	19.94	5482	CG MET A 820	38.153	7.749	45.900	1.00	22.93
5438	CB ASP A 815	42.555	13.118	54.789	1.00	17.34	5483	SD MET A 820	36.405	8.041	45.961	1.00	23.93
5439	CG ASP A 815	43.531	13.119	55.974	1.00	20.48	5484	CE MET A 820	36.118	9.783	45.834	1.00	23.13
5440	OD1 ASP A 815	44.579	12.408	55.987	1.00	19.52	5485	N ILE A 821	40.688	5.642	48.244	1.00	17.40

5576	CB	ARG A 831	37.362	-4.574	42.188	1.00	16.96	5621	O	GLN A 837	28.053	-7.047	35.906	1.00	17.00
5577	CG	ARG A 831	38.080	-3.419	42.858	1.00	16.46	5622	CB	GLN A 837	30.603	-8.904	36.400	1.00	21.90
5578	CD	ARG A 831	38.971	-3.779	44.005	1.00	17.94	5623	CG	GLN A 837	30.712	-10.131	37.263	1.00	22.49
5579	NE	ARG A 831	38.365	-3.942	45.328	1.00	17.80	5624	CD	GLN A 837	31.790	-9.982	38.343	1.00	21.99
5580	CG	ARG A 831	38.198	-5.082	45.971	1.00	18.41	5625	OE1	GLN A 837	32.918	-9.616	38.024	1.00	20.17
5581	NH1	ARG A 831	38.542	-6.244	45.421	1.00	18.63	5626	NE2	GLN A 837	31.367	-10.297	39.564	1.00	20.64
5582	NH2	ARG A 831	37.617	-5.115	47.169	1.00	18.47	5627	N	ILE A 838	29.898	-6.608	34.623	1.00	16.54
5583	N	MET A 832	34.819	-5.468	39.649	1.00	16.98	5628	CA	ILE A 838	29.667	-5.167	34.499	1.00	18.19
5584	CA	MET A 832	34.280	-6.623	38.923	1.00	16.56	5629	C	ILE A 838	28.370	-4.877	33.740	1.00	20.92
5585	C	MET A 832	35.367	-7.141	37.961	1.00	17.92	5630	O	ILE A 838	27.578	-3.998	34.152	1.00	18.47
5586	O	MET A 832	36.184	-6.323	37.488	1.00	17.69	5631	CB	ILE A 838	30.895	-4.516	33.835	1.00	19.11
5587	CB	MET A 832	33.002	-6.169	38.210	1.00	16.53	5632	CG1	ILE A 838	32.141	-4.578	34.778	1.00	16.48
5588	CG	MET A 832	31.834	-5.953	39.241	1.00	15.93	5633	CG2	ILE A 838	30.618	-3.062	33.428	1.00	18.17
5589	SD	MET A 832	30.273	-5.680	38.352	1.00	14.50	5634	CD1	ILE A 838	33.422	-4.259	33.992	1.00	16.81
5590	CE	MET A 832	30.215	-3.878	38.401	1.00	13.68	5635	N	LYS A 839	28.126	-5.604	32.642	1.00	20.40
5591	N	THR A 833	35.416	-8.440	37.714	1.00	16.30	5636	CA	LYS A 839	26.868	-5.425	31.895	1.00	24.05
5592	CA	THR A 833	36.465	-8.992	36.872	1.00	17.66	5637	C	LYS A 839	25.681	-5.781	32.770	1.00	25.13
5593	C	THR A 833	36.119	-9.364	35.440	1.00	19.22	5638	O	LYS A 839	24.646	-5.116	32.756	1.00	26.96
5594	O	THR A 833	37.057	-9.531	34.621	1.00	17.30	5639	CB	LYS A 839	26.836	-6.328	30.636	1.00	24.14
5595	CB	THR A 833	37.064	-10.227	37.580	1.00	17.12	5640	CD	LYS A 839	27.894	-5.833	29.641	1.00	26.39
5596	CG1	THR A 833	36.053	-11.222	37.737	1.00	18.20	5641	CD	LYS A 839	27.580	-6.351	28.235	1.00	30.49
5597	CG2	THR A 833	37.634	-9.883	38.959	1.00	16.91	5642	CE	LYS A 839	28.219	-7.705	28.025	1.00	32.93
5598	N	THR A 834	34.820	-9.464	35.089	1.00	17.86	5643	NZ	LYS A 839	28.865	-7.658	26.661	1.00	35.80
5599	CA	THR A 834	34.456	-9.796	33.723	1.00	19.46	5644	N	GLN A 840	25.788	-6.819	33.588	1.00	25.00
5600	C	THR A 834	33.566	-8.753	33.065	1.00	18.40	5645	CA	GLN A 840	24.684	-7.184	34.471	1.00	26.52
5601	O	THR A 834	32.831	-8.051	33.768	1.00	18.40	5646	C	GLN A 840	24.438	-6.235	35.642	1.00	24.27
5602	CB	THR A 834	33.710	-11.144	33.592	1.00	19.44	5647	O	GLN A 840	23.285	-6.041	36.067	1.00	21.92
5603	CG1	THR A 834	32.393	-10.968	34.125	1.00	20.68	5648	CB	GLN A 840	25.070	-8.548	35.028	1.00	31.74
5604	CG2	THR A 834	34.421	-12.276	34.309	1.00	19.43	5649	CG	GLN A 840	23.972	-9.403	35.610	1.00	39.43
5605	N	ALA A 835	33.566	-8.699	31.732	1.00	19.48	5650	CD	GLN A 840	24.253	-10.889	35.404	1.00	43.34
5606	CA	ALA A 835	32.648	-7.803	31.033	1.00	20.00	5651	OE1	GLN A 840	23.875	-11.733	36.232	1.00	45.14
5607	C	ALA A 835	31.193	-8.165	31.312	1.00	20.77	5652	NE2	GLN A 840	24.920	-11.257	34.306	1.00	44.87
5608	O	ALA A 835	30.385	-7.248	31.410	1.00	22.50	5653	N	ASN A 841	25.494	-5.678	36.234	1.00	17.07
5609	CB	ALA A 835	32.842	-7.825	29.508	1.00	18.74	5654	CA	ASN A 841	25.352	-4.940	37.483	1.00	19.33
5610	N	ASP A 836	30.790	-9.421	31.421	1.00	22.07	5655	C	ASN A 841	25.456	-3.442	37.474	1.00	17.58
5611	CA	ASP A 836	29.447	-9.864	31.696	1.00	23.30	5656	O	ASN A 841	25.171	-2.831	38.520	1.00	17.51
5612	C	ASP A 836	28.969	-9.388	33.066	1.00	21.99	5657	CB	ASN A 841	26.468	-5.479	38.436	1.00	20.01
5613	O	ASP A 836	27.808	-9.041	33.223	1.00	22.47	5658	CG	ASN A 841	26.318	-6.928	38.823	1.00	21.30
5614	CB	ASP A 836	29.282	-11.410	31.664	1.00	25.61	5659	OD1	ASN A 841	27.336	-7.581	39.153	1.00	24.17
5615	CG	ASP A 836	29.189	-11.927	30.230	1.00	27.82	5660	NH2	ASN A 841	25.136	-7.506	38.867	1.00	17.31
5616	OD1	ASP A 836	29.351	-13.150	30.024	1.00	30.02	5661	N	LEU A 842	25.969	-2.825	36.425	1.00	17.66
5617	OD2	ASP A 836	29.058	-11.147	29.276	1.00	26.35	5662	CA	LEU A 842	26.184	-1.376	36.377	1.00	17.63
5618	N	GLN A 837	29.844	-9.310	34.063	1.00	21.84	5663	C	LEU A 842	25.163	-0.724	35.461	1.00	18.99
5619	CA	GLN A 837	29.453	-8.854	35.377	1.00	20.02	5664	O	LEU A 842	25.011	-1.186	34.306	1.00	17.85
5620	C	GLN A 837	29.051	-7.386	35.296	1.00	10.66	5665	CB	LRO A 842	27.657	-1.086	35.967	1.00	16.31

5666	CG	LEU	A	842	28.122	0.412	36.099	1.00	16.16	5711	CA	PRO	A	848	21.738	16.711	34.326	1.00	21.84
5667	CD1	LEU	A	842	29.646	0.464	36.201	1.00	15.40	5712	C	PRO	A	848	22.900	16.792	33.349	1.00	24.33
5668	CD2	LEU	A	842	27.670	1.171	34.847	1.00	16.66	5713	O	PRO	A	848	23.896	16.064	33.439	1.00	22.58
5669	N	THR	A	843	24.433	0.335	35.896	1.00	18.55	5714	CB	PRO	A	848	21.911	17.756	35.428	1.00	21.32
5670	CA	THR	A	843	23.509	0.996	34.955	1.00	19.55	5715	CG	PRO	A	848	21.153	17.200	36.614	1.00	21.13
5671	C	THR	A	843	23.799	2.485	35.083	1.00	18.14	5716	CD	PRO	A	848	21.503	15.705	36.538	1.00	20.99
5672	O	THR	A	843	23.954	2.940	36.217	1.00	18.37	5717	N	THR	A	849	22.785	17.738	32.406	1.00	24.17
5673	CB	THR	A	843	21.997	0.715	35.324	1.00	21.75	5718	CA	THR	A	849	23.849	17.972	31.424	1.00	24.95
5674	OG1	THR	A	843	21.984	0.728	36.780	1.00	27.30	5719	C	THR	A	849	25.242	18.088	32.050	1.00	22.16
5675	CG2	THR	A	843	21.591	-0.733	35.145	1.00	20.25	5720	O	THR	A	849	25.493	18.737	33.071	1.00	21.14
5676	N	PHE	A	844	23.800	3.289	34.050	1.00	17.73	5721	CB	THR	A	849	23.540	19.287	30.661	1.00	24.81
5677	CA	PHE	A	844	23.831	4.740	34.087	1.00	17.70	5722	OG1	THR	A	849	22.271	19.114	30.029	1.00	25.94
5678	C	PHE	A	844	22.432	5.276	34.395	1.00	19.50	5723	CG2	THR	A	849	24.626	19.557	29.609	1.00	25.93
5679	O	PHE	A	844	21.404	4.713	33.999	1.00	17.81	5724	N	ASN	A	850	26.201	17.420	31.423	1.00	20.59
5680	CB	PHE	A	844	24.393	5.290	32.769	1.00	19.16	5725	CA	ASN	A	850	27.600	17.432	31.834	1.00	20.77
5681	CG	PHE	A	844	25.890	4.994	32.659	1.00	18.93	5726	C	ASN	A	850	27.795	16.847	33.239	1.00	19.84
5682	CD1	PHE	A	844	26.336	3.998	31.778	1.00	19.58	5727	O	ASN	A	850	28.665	17.266	34.020	1.00	18.02
5683	CD2	PHE	A	844	26.805	5.688	33.423	1.00	16.70	5728	CB	ASN	A	850	28.286	18.778	31.664	1.00	20.31
5684	CE1	PHE	A	844	27.691	3.718	31.666	1.00	17.53	5729	CG	ASN	A	850	29.817	18.702	31.663	1.00	21.52
5685	CE2	PHE	A	844	28.161	5.407	33.322	1.00	16.61	5730	OD1	ASN	A	850	30.384	17.768	31.100	1.00	19.79
5686	CZ	PHE	A	844	28.604	4.408	32.474	1.00	16.03	5731	N	ASN	A	850	30.504	19.668	32.261	1.00	18.52
5687	N	LEU	A	845	22.317	6.283	35.262	1.00	20.29	5732	N	THR	A	851	27.040	15.769	33.508	1.00	18.54
5688	CA	LEU	A	845	21.038	6.840	35.660	1.00	21.27	5733	CA	THR	A	851	27.234	14.985	34.728	1.00	19.54
5689	C	LEU	A	845	20.919	8.200	34.954	1.00	23.53	5734	C	THR	A	851	27.138	13.496	34.402	1.00	19.84
5690	O	LEU	A	845	21.935	8.833	34.636	1.00	23.88	5735	O	THR	A	851	26.541	13.150	33.375	1.00	18.01
5691	CB	LEU	A	845	20.935	7.051	37.170	1.00	21.66	5736	CB	THR	A	851	26.235	15.237	35.873	1.00	18.24
5692	CG	LEU	A	845	21.162	5.826	38.092	1.00	23.12	5737	OG1	THR	A	851	24.907	14.853	35.442	1.00	20.28
5693	CD1	LEU	A	845	21.274	6.272	39.546	1.00	22.17	5738	CG2	THR	A	851	26.248	16.692	36.320	1.00	18.83
5694	CD2	LEU	A	845	20.052	4.791	37.920	1.00	23.11	5739	N	VAL	A	852	27.723	12.627	35.230	1.00	18.35
5695	N	GLU	A	846	19.690	8.626	34.698	1.00	21.38	5740	CA	VAL	A	852	27.673	11.190	34.978	1.00	18.50
5696	CA	GLU	A	846	19.490	9.929	34.070	1.00	24.30	5741	C	VAL	A	852	27.277	10.516	36.296	1.00	19.16
5697	C	GLU	A	846	19.991	11.035	34.975	1.00	21.71	5742	O	VAL	A	852	28.012	10.724	37.365	1.00	16.89
5698	O	GLU	A	846	19.653	11.010	36.172	1.00	20.11	5743	CB	VAL	A	852	29.064	10.638	34.571	1.00	20.21
5699	CG	GLU	A	846	17.975	10.166	33.842	1.00	28.61	5744	CG1	VAL	A	852	29.058	9.112	34.604	1.00	18.62
5700	CD	GLU	A	846	17.724	11.373	32.965	1.00	34.76	5745	CG2	VAL	A	852	29.530	11.124	33.192	1.00	17.86
5701	CD	GLU	A	846	17.726	12.749	33.588	1.00	39.53	5746	N	ALA	A	853	26.272	9.662	36.315	1.00	17.66
5702	OE1	GLU	A	846	18.229	13.687	32.884	1.00	41.56	5747	CA	ALA	A	853	25.839	8.989	37.544	1.00	16.64
5703	OE2	GLU	A	846	17.272	13.005	34.732	1.00	40.66	5748	C	ALA	A	853	25.511	7.540	37.210	1.00	17.67
5704	N	SER	A	847	20.680	12.026	34.430	1.00	19.82	5749	O	ALA	A	853	24.951	7.276	36.117	1.00	18.63
5705	CA	SER	A	847	21.208	13.081	35.319	1.00	18.64	5750	CB	ALA	A	853	24.565	9.709	38.039	1.00	15.15
5706	C	SER	A	847	21.368	14.319	34.462	1.00	19.77	5751	N	PHE	A	854	25.863	6.606	38.068	1.00	16.51
5707	O	SER	A	847	21.263	14.210	33.233	1.00	13.46	5752	CA	PHE	A	854	25.701	5.180	37.832	1.00	17.75
5708	CB	SER	A	847	22.527	12.667	36.002	1.00	17.95	5753	C	PHE	A	854	25.400	4.431	39.126	1.00	18.33
5709	OG	SER	A	847	23.592	12.595	35.047	1.00	19.81	5754	O	PHE	A	854	26.573	4.950	40.251	1.00	19.36
5710	N	PRO	A	848	21.622	15.466	35.068	1.00	20.84	5755	CB	PHE	A	854	26.922	4.577	37.103	1.00	18.03

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5756	CG	PHE A 854	28.266	4.665	37.791	1.00	18.64	5801	CG	TYR A 859	24.243	-7.457	48.362	1.00	18.89
5757	CD1	PHE A 854	28.705	3.655	38.635	1.00	19.06	5802	CD1	TYR A 859	22.870	-7.641	48.244	1.00	20.51
5758	CD2	PHE A 854	29.117	5.734	37.569	1.00	18.31	5803	CD2	TYR A 859	24.719	-6.915	49.548	1.00	17.97
5759	CE1	PHE A 854	29.952	3.745	39.251	1.00	17.32	5804	CE1	TYR A 859	21.995	-7.319	49.262	1.00	20.07
5760	CE2	PHE A 854	30.366	5.799	38.148	1.00	17.33	5805	CE2	TYR A 859	23.860	-6.602	50.574	1.00	18.09
5761	CZ	PHE A 854	30.793	4.792	39.003	1.00	15.66	5806	CZ	TYR A 859	22.496	-6.786	50.428	1.00	21.56
5762	N	GLU A 855	24.837	3.226	38.985	1.00	18.41	5807	OH	TYR A 859	21.657	-6.473	51.472	1.00	20.57
5763	CA	GLU A 855	24.385	2.432	40.134	1.00	18.15	5808	N	ALA A 860	26.756	-6.405	44.195	1.00	14.63
5764	C	GLU A 855	24.952	1.008	40.033	1.00	17.60	5809	CA	ALA A 860	27.573	-6.753	43.030	1.00	16.97
5765	O	GLU A 855	25.011	0.485	38.900	1.00	15.72	5810	C	ALA A 860	28.955	-7.249	43.442	1.00	18.77
5766	CB	GLU A 855	22.839	2.373	40.213	1.00	17.57	5811	O	ALA A 860	29.597	-6.651	44.336	1.00	19.26
5767	CG	GLU A 855	22.296	1.628	41.437	1.00	18.25	5812	CB	ALA A 860	27.744	-5.511	42.164	1.00	18.48
5768	CD	GLU A 855	20.756	1.617	41.583	1.00	21.29	5813	N	ASN A 861	29.362	-8.365	42.860	1.00	18.35
5769	OE1	GLU A 855	20.194	1.168	42.603	1.00	18.85	5814	CA	ASN A 861	30.655	-8.995	43.164	1.00	18.84
5770	OE2	GLU A 855	20.095	2.079	40.611	1.00	22.94	5815	C	ASN A 861	30.855	-9.139	44.672	1.00	19.08
5771	N	LEU A 856	25.606	0.580	41.096	1.00	17.21	5816	O	ASN A 861	31.935	-8.866	45.226	1.00	18.01
5772	CA	LEU A 856	26.188	-0.794	41.188	1.00	18.95	5817	CB	ASN A 861	31.796	-8.205	42.485	1.00	18.52
5773	C	LEU A 856	25.172	-1.634	41.962	1.00	18.66	5818	CG	ASN A 861	33.144	-8.920	42.430	1.00	18.65
5774	O	LEU A 856	24.868	-1.303	43.156	1.00	20.65	5819	OD1	ASN A 861	33.182	-10.129	42.202	1.00	18.09
5775	CB	LEU A 856	27.582	-0.729	41.838	1.00	15.58	5820	ND2	ASN A 861	34.255	-8.206	42.638	1.00	16.42
5776	CG	LEU A 856	28.600	0.261	41.242	1.00	15.91	5821	N	HIS A 862	29.923	-9.745	45.420	1.00	18.36
5777	CD1	LEU A 856	29.935	0.194	42.026	1.00	15.73	5822	CA	HIS A 862	29.912	-10.026	46.835	1.00	18.01
5778	CD2	LEU A 856	28.851	-0.034	39.762	1.00	15.55	5823	C	HIS A 862	30.326	-8.786	47.655	1.00	18.23
5779	N	LYS A 857	24.482	-2.559	41.308	1.00	20.01	5824	O	HIS A 862	31.071	-8.845	48.634	1.00	19.60
5780	CA	LYS A 857	23.349	-3.244	41.916	1.00	21.47	5825	CB	HIS A 862	30.725	-11.267	47.307	1.00	18.46
5781	C	LYS A 857	23.415	-4.614	42.559	1.00	19.85	5826	CG	HIS A 862	32.194	-11.226	46.999	1.00	20.04
5782	O	LYS A 857	24.129	-5.512	42.141	1.00	16.38	5827	ND1	HIS A 862	32.690	-11.802	45.836	1.00	21.25
5783	CB	LYS A 857	22.273	-3.433	40.784	1.00	23.29	5828	CD2	HIS A 862	33.279	-10.559	47.560	1.00	21.51
5784	CG	LYS A 857	21.724	-2.106	40.284	1.00	26.57	5829	CE1	HIS A 862	33.983	-11.616	45.725	1.00	21.85
5785	CD	LYS A 857	20.895	-2.342	38.990	1.00	28.26	5830	NE2	HIS A 862	34.380	-10.896	46.767	1.00	23.07
5786	CE	LYS A 857	21.874	-2.829	37.915	1.00	29.07	5831	N	ASP A 863	29.770	-7.637	47.354	1.00	16.12
5787	NZ	LYS A 857	21.301	-3.488	36.718	1.00	28.50	5832	CA	ASP A 863	29.883	-6.424	48.130	1.00	17.57
5788	N	ASN A 858	22.551	-4.779	43.556	1.00	20.08	5833	C	ASP A 863	28.980	-6.498	49.361	1.00	16.17
5789	CA	ASN A 858	22.342	-6.017	44.296	1.00	22.03	5834	O	ASP A 863	27.999	-7.241	49.361	1.00	15.89
5790	C	ASN A 858	23.574	-6.787	44.771	1.00	19.15	5835	CB	ASP A 863	29.435	-5.250	47.242	1.00	17.41
5791	O	ASN A 858	23.832	-7.961	44.451	1.00	17.47	5836	CG	ASP A 863	30.045	-3.935	47.687	1.00	19.24
5792	CB	ASN A 858	21.481	-6.963	43.428	1.00	24.99	5837	OD1	ASP A 863	31.158	-3.597	47.207	1.00	15.53
5793	CG	ASN A 858	20.672	-7.932	44.294	1.00	27.08	5838	OD2	ASP A 863	29.459	-3.191	48.509	1.00	20.34
5794	OD1	ASN A 858	20.308	-7.642	45.418	1.00	25.89	5839	N	THR A 864	29.270	-5.700	50.388	1.00	16.93
5795	ND2	ASN A 858	20.346	-9.104	43.726	1.00	28.26	5840	CA	THR A 864	28.442	-5.615	51.570	1.00	17.66
5796	N	TYR A 859	24.290	-6.198	45.719	1.00	15.00	5841	C	THR A 864	27.315	-4.585	51.445	1.00	19.37
5797	CA	TYR A 859	25.524	-6.732	46.272	1.00	15.84	5842	O	THR A 864	26.382	-4.558	52.256	1.00	19.59
5798	C	TYR A 859	26.470	-7.231	45.162	1.00	14.81	5843	CB	THR A 864	29.230	-5.242	52.846	1.00	18.03
5799	O	TYR A 859	26.871	-8.386	45.149	1.00	13.23	5844	OG1	THR A 864	30.031	-4.081	52.545	1.00	18.52
5800	CB	TYR A 859	25.147	-7.865	47.215	1.00	17.53	5845	CG2	THR A 864	30.062	-6.428	51.337	1.00	17.90

5846	N	TRP	A	865	27.378	-3.754	50.419	1.00	18.22	5891	CG2	ILE	A	869	24.060	7.342	42.951	1.00	14.77
5847	CA	TRP	A	865	26.366	-2.703	50.191	1.00	19.88	5892	CD1	ILE	A	869	21.309	5.688	43.251	1.00	17.74
5848	C	TRP	A	865	25.478	-3.241	49.072	1.00	21.10	5893	N	VAL	A	870	27.084	6.345	42.385	1.00	13.11
5849	O	TRP	A	865	25.965	-3.703	48.039	1.00	19.83	5894	CA	VAL	A	870	28.208	7.276	42.308	1.00	15.88
5850	CB	TRP	A	865	27.055	-1.385	49.070	1.00	20.11	5895	C	VAL	A	870	27.777	8.403	41.357	1.00	13.78
5851	CG	TRP	A	865	27.697	-0.603	50.975	1.00	20.00	5896	O	VAL	A	870	27.303	8.071	40.277	1.00	14.36
5852	CD1	TRP	A	865	27.512	-0.899	52.310	1.00	20.46	5897	CB	VAL	A	870	29.500	6.597	41.787	1.00	16.19
5853	CD2	TRP	A	865	28.490	0.608	50.952	1.00	19.16	5898	CG1	VAL	A	870	30.634	7.584	41.464	1.00	17.02
5854	NE1	TRP	A	865	28.207	-0.016	53.072	1.00	19.59	5899	CG2	VAL	A	870	29.989	5.575	42.045	1.00	15.31
5855	CE2	TRP	A	865	28.808	0.918	52.281	1.00	20.04	5900	N	MET	A	871	28.093	9.657	41.556	1.00	15.32
5856	CE3	TRP	A	865	29.016	1.392	49.936	1.00	18.40	5901	CA	MET	A	871	27.849	10.659	40.508	1.00	16.32
5857	CZ2	TRP	A	865	29.584	2.019	52.639	1.00	19.58	5902	C	MET	A	871	28.985	11.671	40.520	1.00	16.77
5858	CZ3	TRP	A	865	29.777	2.502	50.287	1.00	20.06	5903	O	MET	A	871	29.341	12.115	41.624	1.00	16.61
5859	CH2	TRP	A	865	30.082	2.782	51.624	1.00	18.82	5904	CB	MET	A	871	26.511	11.402	40.645	1.00	17.18
5860	N	LYS	A	866	24.171	-3.257	49.278	1.00	18.45	5905	CG	MET	A	871	26.303	12.711	39.875	1.00	18.06
5861	CA	LYS	A	866	23.184	-3.732	48.319	1.00	20.04	5906	SD	MET	A	871	24.576	13.307	40.042	1.00	17.89
5862	C	LYS	A	866	23.133	-2.967	47.004	1.00	19.12	5907	CE	MET	A	871	24.717	14.958	39.345	1.00	17.65
5863	O	LYS	A	866	23.316	-3.533	45.926	1.00	16.16	5908	N	TYR	A	872	29.496	11.964	39.333	1.00	15.67
5864	CB	LYS	A	866	21.813	-3.689	49.002	1.00	20.09	5909	CA	TYR	A	872	30.520	13.001	39.181	1.00	17.64
5865	CG	LYS	A	866	20.635	-4.165	48.181	1.00	25.35	5910	C	TYR	A	872	29.866	14.313	38.765	1.00	17.57
5866	CD	LYS	A	866	19.462	-4.533	49.094	1.00	30.56	5911	O	TYR	A	872	29.125	14.271	37.786	1.00	16.70
5867	CE	LYS	A	866	18.162	-4.133	48.385	1.00	32.55	5912	CB	TYR	A	872	31.569	12.699	38.081	1.00	16.70
5868	NZ	LYS	A	866	17.703	-5.263	47.516	1.00	36.93	5913	CG	TYR	A	872	32.156	11.318	38.208	1.00	16.28
5869	N	ASN	A	867	22.957	-1.640	47.085	1.00	17.81	5914	CD1	TYR	A	872	32.120	10.472	37.110	1.00	13.82
5870	CA	ASN	A	867	22.992	-0.817	45.878	1.00	19.57	5915	CD2	TYR	A	872	32.651	10.833	39.432	1.00	17.04
5871	C	ASN	A	867	23.954	0.339	46.119	1.00	19.05	5916	CE1	TYR	A	872	32.631	9.180	37.193	1.00	15.56
5872	O	ASN	A	867	23.947	0.830	47.255	1.00	17.99	5917	CE2	TYR	A	872	33.138	9.522	39.527	1.00	16.23
5873	CB	ASN	A	867	21.656	-0.244	45.428	1.00	19.15	5918	CZ	TYR	A	872	33.069	8.596	38.405	1.00	16.02
5874	CG	ASN	A	867	20.650	-1.322	45.045	1.00	20.68	5919	OH	TYR	A	872	33.528	7.402	38.433	1.00	16.10
5875	OD1	ASN	A	867	20.987	-2.249	44.295	1.00	20.32	5920	N	ASN	A	873	30.114	15.425	39.416	1.00	18.25
5876	ND2	ASN	A	867	19.422	-1.255	45.549	1.00	17.97	5921	CA	ASN	A	873	29.599	16.720	39.021	1.00	17.41
5877	N	ILE	A	868	24.751	0.805	45.213	1.00	18.06	5922	C	ASN	A	873	30.804	17.644	38.874	1.00	17.53
5878	CA	ILE	A	868	25.644	1.902	45.360	1.00	17.77	5923	O	ASN	A	873	31.181	18.240	39.867	1.00	18.67
5879	C	ILE	A	868	25.425	2.872	44.217	1.00	17.69	5924	CB	ASN	A	873	28.650	17.362	40.055	1.00	18.79
5880	O	ILE	A	868	25.330	2.391	43.094	1.00	18.10	5925	CG	ASN	A	873	28.169	18.759	39.681	1.00	19.71
5881	CB	ILE	A	868	27.127	1.424	45.318	1.00	18.75	5926	OD1	ASN	A	873	28.219	19.179	38.513	1.00	19.99
5882	CG1	ILE	A	868	27.433	0.426	46.467	1.00	19.10	5927	ND2	ASN	A	873	27.768	19.612	40.630	1.00	16.40
5883	CG2	ILE	A	868	28.041	2.639	45.602	1.00	18.17	5928	N	PRO	A	874	31.324	17.850	37.673	1.00	17.92
5884	CD1	ILE	A	868	28.866	-0.183	46.382	1.00	19.08	5929	CA	PRO	A	874	32.426	18.758	37.448	1.00	18.85
5885	N	ILE	A	869	25.397	4.154	44.510	1.00	16.22	5930	C	PRO	A	874	31.964	20.201	37.260	1.00	20.43
5886	CA	ILE	A	869	25.256	5.150	43.447	1.00	15.16	5931	O	PRO	A	874	32.857	21.062	37.114	1.00	19.83
5887	C	ILE	A	869	26.496	6.039	43.528	1.00	15.96	5932	CB	PRO	A	874	33.028	18.250	36.120	1.00	18.54
5888	O	ILE	A	869	26.936	6.880	44.637	1.00	17.68	5933	CG	PRO	A	874	31.814	17.776	36.350	1.00	18.34
5889	CB	ILE	A	869	23.932	5.949	43.590	1.00	14.79	5934	CD	PRO	A	874	30.927	17.154	36.432	1.00	18.38
5890	CG1	ILE	A	869	22.753	5.177	43.024	1.00	16.18	5935	N	ASN	A	875	30.658	20.187	37.266	1.00	18.81

5936	CA	ASN A 875	30.197	21.862	37.056	1.00	21.71	5981	N	LEU A 881	20.041	15.196	41.424	1.00	17.50
5937	C	ASN A 875	30.401	22.836	38.198	1.00	21.33	5982	CA	LEU A 881	19.883	13.866	40.872	1.00	17.31
5938	O	ASN A 875	30.422	22.397	39.369	1.00	20.55	5983	C	LEU A 881	18.575	13.262	41.401	1.00	17.89
5939	CB	ASN A 875	28.687	21.786	36.701	1.00	22.52	5984	O	LEU A 881	18.363	13.335	42.617	1.00	17.14
5940	CG	ASN A 875	28.451	20.853	35.519	1.00	24.12	5985	CB	LEU A 881	21.058	12.982	41.365	1.00	18.29
5941	OD1	ASN A 875	28.894	21.182	34.417	1.00	26.00	5986	CG	LEU A 881	21.001	11.492	41.039	1.00	20.54
5942	ND2	ASN A 875	27.799	19.711	35.664	1.00	21.36	5987	CD1	LEU A 881	21.214	11.106	39.528	1.00	21.58
5943	N	LYS A 876	30.486	24.146	37.974	1.00	21.86	5988	CD2	LEU A 881	22.087	10.899	41.817	1.00	20.54
5944	CA	LYS A 876	30.645	25.159	39.028	1.00	25.54	5989	N	ASN A 882	17.745	12.668	40.578	1.00	18.74
5945	C	LYS A 876	29.380	25.447	39.861	1.00	23.68	5990	CA	ASN A 882	16.529	11.983	40.974	1.00	20.32
5946	O	LYS A 876	29.408	26.291	40.768	1.00	20.96	5991	C	ASN A 882	16.916	10.547	41.262	1.00	19.51
5947	CB	LYS A 876	31.049	26.536	38.435	1.00	28.74	5992	O	ASN A 882	17.686	9.944	40.505	1.00	21.26
5948	CG	LYS A 876	32.446	26.518	37.768	1.00	32.96	5993	CB	ASN A 882	15.547	12.040	39.832	1.00	24.52
5949	CD	LYS A 876	33.382	26.138	38.926	1.00	35.88	5994	CG	ASN A 882	15.024	13.451	39.705	1.00	27.48
5950	CE	LYS A 876	34.570	27.098	39.033	1.00	37.37	5995	OD1	ASN A 882	14.600	14.087	40.666	1.00	28.76
5951	NZ	LYS A 876	35.469	26.778	37.875	1.00	36.83	5996	ND2	ASN A 882	15.063	13.946	38.456	1.00	20.00
5952	N	THR A 877	28.261	24.779	39.591	1.00	22.70	5997	N	LEU A 883	16.404	9.998	42.341	1.00	20.69
5953	CA	THR A 877	27.057	24.946	40.425	1.00	22.49	5998	CA	LEU A 883	16.795	8.686	42.799	1.00	19.88
5954	C	THR A 877	26.579	23.547	40.821	1.00	21.81	5999	C	LEU A 883	15.783	7.565	42.619	1.00	21.80
5955	O	THR A 877	26.865	22.555	40.163	1.00	19.74	6000	O	LEU A 883	14.583	7.773	42.723	1.00	23.04
5956	CB	THR A 877	25.891	25.589	39.673	1.00	23.36	6001	CB	LEU A 883	17.076	8.771	44.330	1.00	19.20
5957	OG1	THR A 877	25.632	24.830	38.499	1.00	23.54	6002	CG	LEU A 883	18.161	9.773	44.743	1.00	19.84
5958	CG2	THR A 877	26.212	27.030	39.271	1.00	25.23	6003	CD1	LEU A 883	18.166	10.045	46.259	1.00	20.56
5959	N	SER A 878	25.857	23.541	41.955	1.00	18.08	6004	CD2	LEU A 883	19.510	9.241	44.291	1.00	15.99
5960	CA	SER A 878	25.326	22.269	42.406	1.00	18.86	6005	N	PRO A 884	16.303	6.364	42.482	1.00	20.55
5961	C	SER A 878	24.284	21.737	41.420	1.00	19.86	6006	CA	PRO A 884	15.498	5.168	42.474	1.00	23.11
5962	O	SER A 878	23.661	22.481	40.673	1.00	18.20	6007	C	PRO A 884	14.757	5.106	43.809	1.00	22.93
5963	CB	SER A 878	24.366	22.598	43.617	1.00	16.87	6008	O	PRO A 884	15.119	5.780	44.796	1.00	21.23
5964	OG	SER A 878	23.469	23.709	43.603	1.00	20.00	6009	CB	PRO A 884	16.530	4.053	42.301	1.00	22.91
5965	N	GLN A 879	24.144	20.400	41.475	1.00	20.32	6010	CG	PRO A 884	17.714	4.713	41.660	1.00	21.54
5966	CA	GLN A 879	23.180	19.790	40.580	1.00	21.86	6011	CD	PRO A 884	17.762	6.046	42.397	1.00	20.96
5967	C	GLN A 879	22.200	18.733	41.224	1.00	22.97	6012	N	SER A 885	13.760	4.240	43.934	1.00	21.66
5968	O	GLN A 879	22.675	18.029	42.131	1.00	21.65	6013	CA	SER A 885	12.967	4.273	45.162	1.00	24.40
5969	CB	GLN A 879	23.931	18.974	39.468	1.00	22.37	6014	C	SER A 885	13.716	3.881	46.431	1.00	23.95
5970	CG	GLN A 879	24.910	19.802	38.645	1.00	22.60	6015	O	SER A 885	14.814	3.285	46.467	1.00	21.34
5971	CD	GLN A 879	24.240	20.815	37.750	1.00	23.49	6016	CB	SER A 885	11.706	3.395	44.996	1.00	25.34
5972	OE1	GLN A 879	23.305	20.445	37.029	1.00	24.49	6017	OG	SER A 885	12.206	2.088	45.063	1.00	26.34
5973	NE2	GLN A 879	24.740	22.035	37.686	1.00	23.81	6018	N	GLY A 886	13.117	4.365	47.544	1.00	21.95
5974	N	THR A 880	20.980	18.539	40.721	1.00	20.70	6019	CA	GLY A 886	13.647	3.960	48.850	1.00	21.89
5975	CA	THR A 880	20.040	17.652	41.394	1.00	21.62	6020	C	GLY A 886	14.483	4.998	49.573	1.00	22.67
5976	C	THR A 880	19.919	16.302	40.713	1.00	18.77	6021	O	GLY A 886	14.689	6.146	49.165	1.00	23.42
5977	O	THR A 880	19.923	16.258	39.513	1.00	18.27	6022	N	ASP A 887	14.869	4.680	50.801	1.00	21.05
5978	CB	THR A 880	18.613	18.275	41.489	1.00	25.07	6023	CA	ASP A 887	15.760	5.451	51.645	1.00	22.50
5979	OG1	THR A 880	18.717	19.445	42.338	1.00	27.52	6024	C	ASP A 887	17.214	5.281	51.210	1.00	20.68
5980	CG2	THR A 880	17.672	17.294	42.200	1.00	26.46	6025	O	ASP A 887	17.634	4.130	51.040	1.00	19.39

6026	CB	ASP	A	887	15.602	4.969	53.086	1.00	23.02	6071	CA	LEU	A	893	29.668	14.397	49.870	1.00	18.16
6027	CG	ASP	A	887	16.484	5.799	54.001	1.00	25.67	6072	C	LEU	A	893	30.721	15.469	50.156	1.00	18.84
6028	OD1	ASP	A	887	17.638	5.419	54.199	1.00	28.60	6073	O	LEU	A	893	31.329	15.577	51.225	1.00	18.84
6029	OD2	ASP	A	887	16.009	6.815	54.502	1.00	20.00	6074	CB	LEU	A	893	28.353	14.725	50.598	1.00	18.93
6030	N	TRP	A	888	17.977	6.376	51.081	1.00	19.72	6075	CG	LEU	A	893	27.657	16.052	50.223	1.00	20.31
6031	CA	TRP	A	888	19.375	6.298	50.691	1.00	17.29	6076	CD1	LEU	A	893	26.160	15.915	50.545	1.00	19.83
6032	C	TRP	A	888	20.292	6.887	51.745	1.00	18.92	6077	CD2	LEU	A	893	28.199	17.314	50.895	1.00	19.07
6033	O	TRP	A	888	19.985	7.977	52.265	1.00	19.35	6078	N	GLY	A	894	30.863	16.384	49.199	1.00	18.44
6034	CB	TRP	A	888	19.584	6.970	49.305	1.00	19.14	6079	CA	GLY	A	894	31.780	17.536	49.376	1.00	19.33
6035	CG	TRP	A	888	19.041	6.188	48.135	1.00	21.37	6080	C	GLY	A	894	33.173	16.936	49.592	1.00	21.53
6036	CD1	TRP	A	888	17.777	6.307	47.614	1.00	19.94	6081	O	GLY	A	894	33.534	16.015	48.857	1.00	20.54
6037	CD2	TRP	A	888	19.692	5.196	47.325	1.00	21.02	6082	N	ASP	A	895	33.906	17.393	50.605	1.00	20.89
6038	NE1	TRP	A	888	17.616	5.449	46.549	1.00	20.33	6083	CA	ASP	A	895	35.240	16.835	50.842	1.00	22.34
6039	CE2	TRP	A	888	18.775	4.742	46.365	1.00	21.10	6084	C	ASP	A	895	35.191	15.680	51.834	1.00	22.18
6040	CE3	TRP	A	888	20.966	4.626	47.345	1.00	23.66	6085	O	ASP	A	895	36.127	15.514	52.615	1.00	24.94
6041	CZ2	TRP	A	888	19.060	3.727	45.435	1.00	20.78	6086	CB	ASP	A	895	36.130	17.947	51.393	1.00	22.12
6042	CZ3	TRP	A	888	21.271	3.645	46.396	1.00	23.95	6087	CG	ASP	A	895	35.478	18.553	52.622	1.00	23.64
6043	CH2	TRP	A	888	20.330	3.181	45.469	1.00	21.41	6088	OD1	ASP	A	895	36.022	19.522	53.153	1.00	25.64
6044	N	THR	A	889	21.444	6.290	52.074	1.00	16.86	6089	OD2	ASP	A	895	34.435	18.052	53.033	1.00	20.00
6045	CA	THR	A	889	22.397	6.862	53.008	1.00	17.70	6090	N	GLN	A	896	34.086	14.968	51.966	1.00	22.81
6046	C	THR	A	889	23.506	7.623	52.293	1.00	18.48	6091	CA	GLN	A	896	33.930	13.925	52.976	1.00	22.65
6047	O	THR	A	889	24.068	7.059	51.330	1.00	17.19	6092	C	GLN	A	896	33.662	12.612	52.237	1.00	22.28
6048	CB	THR	A	889	23.071	5.754	53.870	1.00	18.89	6093	O	GLN	A	896	32.744	12.496	51.436	1.00	19.57
6049	OG1	THR	A	889	22.031	5.014	54.495	1.00	19.06	6094	CB	GLN	A	896	32.781	14.173	53.958	1.00	24.18
6050	CG2	THR	A	889	23.995	6.360	54.928	1.00	16.36	6095	CG	GLN	A	896	32.835	15.288	54.933	1.00	28.13
6051	N	ILE	A	890	23.827	8.864	52.643	1.00	17.13	6096	CD	GLN	A	896	32.024	15.444	56.200	1.00	30.70
6052	CA	ILE	A	890	24.908	9.575	51.956	1.00	18.82	6097	OE1	GLN	A	896	32.333	15.046	57.385	1.00	31.20
6053	C	ILE	A	890	26.259	9.160	52.591	1.00	18.09	6098	NE2	GLN	A	896	30.906	16.146	56.043	1.00	23.23
6054	O	ILE	A	890	26.349	9.198	53.816	1.00	18.88	6099	N	ILE	A	897	34.546	11.646	52.545	1.00	20.05
6055	CB	ILE	A	890	24.732	11.089	52.093	1.00	18.96	6100	CA	ILE	A	897	34.366	10.348	51.925	1.00	19.25
6056	CG1	ILE	A	890	23.367	11.573	51.535	1.00	19.44	6101	C	ILE	A	897	34.674	9.206	53.003	1.00	17.61
6057	CG2	ILE	A	890	25.920	11.771	51.420	1.00	15.34	6102	O	ILE	A	897	35.565	9.391	53.822	1.00	17.24
6058	CD1	ILE	A	890	23.069	12.988	52.057	1.00	19.01	6103	CB	ILE	A	897	35.364	9.778	50.777	1.00	21.18
6059	N	VAL	A	891	27.241	8.700	51.844	1.00	17.95	6104	CG1	ILE	A	897	35.494	11.058	49.949	1.00	19.62
6060	CA	VAL	A	891	28.536	8.307	52.362	1.00	17.49	6105	CG2	ILE	A	897	34.751	8.892	49.874	1.00	24.68
6061	C	VAL	A	891	29.719	9.089	51.748	1.00	17.57	6106	CD1	ILE	A	897	34.203	10.877	49.148	1.00	20.00
6062	O	VAL	A	891	30.808	9.192	52.354	1.00	16.92	6107	N	GLY	A	898	33.824	8.166	53.012	1.00	18.75
6063	CB	VAL	A	891	28.904	6.821	52.307	1.00	18.15	6108	CA	GLY	A	898	34.047	7.122	53.993	1.00	19.72
6064	CG1	VAL	A	891	27.983	6.048	53.233	1.00	19.10	6109	C	GLY	A	898	32.917	6.112	54.045	1.00	21.21
6065	CG2	VAL	A	891	28.997	6.205	50.921	1.00	18.18	6110	O	GLY	A	898	32.131	6.024	53.098	1.00	22.52
6066	N	GLY	A	892	29.413	9.810	50.684	1.00	14.68	6111	N	GLU	A	899	32.839	5.374	55.134	1.00	22.66
6067	CA	GLY	A	892	30.419	10.659	50.046	1.00	15.77	6112	CA	GLU	A	899	31.848	4.331	55.295	1.00	24.68
6068	C	GLY	A	892	29.792	12.007	49.641	1.00	18.34	6113	C	GLU	A	899	30.672	4.756	56.173	1.00	25.01
6069	O	GLY	A	892	28.876	11.911	48.821	1.00	15.50	6114	O	GLU	A	899	29.690	4.011	56.229	1.00	25.22
6070	N	LEU	A	893	30.225	13.102	50.237	1.00	17.98	6115	CB	GLU	A	899	32.539	3.087	55.883	1.00	25.95

6151	CB	VAL A 905	18.271	12.035	50.716	1.00 22.34
6162	CG1 VAL A 905	19.182	13.071	51.320	1.00 22.74	
6163	CG2 VAL A 905	19.108	11.151	49.778	1.00 22.37	
6164	N MET A 906	15.637	10.699	50.260	1.00 21.77	
6165	CA MET A 906	14.755	9.959	49.363	1.00 24.07	
6166	C MET A 906	14.160	10.924	48.328	1.00 23.61	
6167	O MET A 906	14.031	12.130	48.524	1.00 22.79	
6168	CB MET A 906	13.578	9.416	50.195	1.00 26.81	
6169	CG MET A 906	12.397	10.208	50.760	1.00 32.84	
6170	SD MET A 906	11.387	9.012	51.643	1.00 20.00	
6171	CE MET A 906	11.948	7.311	51.468	1.00 20.00	
6172	N GLY A 907	13.907	10.353	47.148	1.00 21.83	
6173	CA GLY A 907	13.278	11.077	46.048	1.00 21.53	
6174	C GLY A 907	14.374	11.725	45.200	1.00 20.44	
6175	O GLY A 907	14.554	11.417	44.029	1.00 18.16	
6176	N ASN A 908	15.070	12.662	45.868	1.00 20.78	
6177	CA ASN A 908	16.156	13.320	45.167	1.00 21.15	
6178	C ASN A 908	17.211	13.868	46.130	1.00 20.98	
6179	O ASN A 908	17.017	13.926	47.338	1.00 18.52	
6180	CB ASN A 908	15.571	14.503	44.390	1.00 25.44	
6181	CG ASN A 908	15.149	15.737	45.145	1.00 20.00	
6182	OD1 ASN A 908	14.950	16.900	44.807	1.00 20.00	
6183	ND2 ASN A 908	14.852	15.267	46.369	1.00 20.00	
6184	N VAL A 909	18.336	14.263	45.507	1.00 18.91	
6185	CA VAL A 909	19.404	14.800	46.327	1.00 18.32	
6186	C VAL A 909	20.288	15.881	45.643	1.00 18.88	
6187	O VAL A 909	20.470	15.801	44.414	1.00 16.18	
6188	CB VAL A 909	20.296	13.598	46.765	1.00 17.97	
6189	CG1 VAL A 909	20.923	12.911	45.546	1.00 19.38	
6190	CG2 VAL A 909	21.470	13.978	47.699	1.00 17.98	
6191	N GLN A 910	20.764	16.892	46.388	1.00 17.12	
6192	CA GLN A 910	21.594	17.918	45.745	1.00 19.67	
6193	C GLN A 910	23.093	17.606	45.891	1.00 20.86	
6194	O GLN A 910	23.536	17.338	47.015	1.00 17.07	
6195	CB GLN A 910	21.229	19.312	46.287	1.00 22.85	
6196	CG GLN A 910	19.856	19.985	46.266	1.00 27.05	
6197	CD GLN A 910	19.701	21.417	46.720	1.00 30.96	
6198	OE1 GLN A 910	20.065	22.155	45.819	1.00 34.28	
6199	NE2 GLN A 910	19.496	21.840	47.984	1.00 20.00	
6200	N VAL A 911	23.796	17.686	44.736	1.00 19.28	
6201	CA VAL A 911	25.245	17.405	44.720	1.00 17.62	
6202	C VAL A 911	26.083	18.669	44.564	1.00 16.72	
6203	O VAL A 911	25.929	19.417	43.604	1.00 15.75	
6204	CB VAL A 911	25.554	16.486	43.522	1.00 18.06	
6205	CG1 VAL A 911	27.073	16.218	43.441	1.00 17.92	

6296	OWO	WAT	W	83	73.802	-6.472	17.967	1.00	11.91	6341	OWO	WAT	W	128	60.874	11.097	38.475	1.00	15.05
6297	OWO	WAT	W	84	63.768	4.437	40.319	1.00	13.88	6342	OWO	WAT	W	129	79.219	-10.342	12.004	1.00	17.14
6298	OWO	WAT	W	85	36.975	5.299	53.120	1.00	17.10	6343	OWO	WAT	W	130	75.096	-14.661	24.693	1.00	15.31
6299	OWO	WAT	W	86	33.546	14.270	46.569	1.00	19.57	6344	OWO	WAT	W	131	73.686	29.364	40.600	1.00	21.16
6300	OWO	WAT	W	87	59.158	9.717	41.808	1.00	15.61	6345	OWO	WAT	W	132	67.581	0.034	15.638	1.00	16.05
6301	OWO	WAT	W	88	41.880	-1.805	42.672	1.00	18.22	6346	OWO	WAT	W	133	70.269	1.088	49.178	1.00	14.16
6302	OWO	WAT	W	89	56.275	9.738	41.533	1.00	13.72	6347	OWO	WAT	W	134	77.523	-12.820	37.177	1.00	13.66
6303	OWO	WAT	W	90	69.059	-23.930	9.758	1.00	20.01	6348	OWO	WAT	W	135	77.079	-2.476	26.781	1.00	22.54
6304	OWO	WAT	W	91	16.344	1.857	52.326	1.00	22.62	6349	OWO	WAT	W	136	44.250	-9.198	31.555	1.00	19.30
6305	OWO	WAT	W	92	75.875	-9.053	49.382	1.00	20.09	6350	OWO	WAT	W	137	43.079	26.840	29.301	1.00	23.07
6306	OWO	WAT	W	93	76.720	-4.117	4.820	1.00	19.57	6351	OWO	WAT	W	138	73.331	-7.883	32.692	1.00	14.37
6307	OWO	WAT	W	94	32.604	16.958	29.686	1.00	15.11	6352	OWO	WAT	W	139	70.346	8.134	44.604	1.00	19.55
6308	OWO	WAT	W	95	14.139	7.588	47.083	1.00	18.86	6353	OWO	WAT	W	140	47.819	9.959	23.729	1.00	19.80
6309	OWO	WAT	W	96	39.342	-8.437	34.765	1.00	18.36	6354	OWO	WAT	W	141	48.447	-8.906	33.755	1.00	15.32
6310	OWO	WAT	W	97	53.612	13.510	41.564	1.00	15.07	6355	OWO	WAT	W	142	29.592	15.853	27.070	1.00	25.10
6311	OWO	WAT	W	98	36.908	-3.575	37.657	1.00	16.19	6356	OWO	WAT	W	143	45.897	-14.006	-16.368	1.00	21.95
6312	OWO	WAT	W	99	81.997	-19.278	2.244	1.00	21.87	6357	OWO	WAT	W	144	65.523	5.063	38.083	1.00	12.12
6313	OWO	WAT	W	100	34.008	1.090	27.119	1.00	17.80	6358	OWO	WAT	W	145	67.211	0.550	32.731	1.00	17.01
6314	OWO	WAT	W	101	56.888	19.001	45.064	1.00	16.05	6359	OWO	WAT	W	146	58.188	15.032	33.459	1.00	18.00
6315	OWO	WAT	W	102	31.113	8.775	55.007	1.00	16.75	6360	OWO	WAT	W	147	56.888	-10.260	18.407	1.00	24.03
6316	OWO	WAT	W	103	68.763	-13.614	32.213	1.00	14.83	6361	OWO	WAT	W	148	89.862	-15.067	24.194	1.00	12.26
6317	OWO	WAT	W	104	77.576	-15.120	38.787	1.00	17.30	6362	OWO	WAT	W	149	66.848	18.769	50.441	1.00	26.40
6318	OWO	WAT	W	105	70.975	9.008	41.415	1.00	15.80	6363	OWO	WAT	W	150	39.850	10.596	24.937	1.00	15.47
6319	OWO	WAT	W	106	73.071	8.260	45.444	1.00	19.77	6364	OWO	WAT	W	151	46.212	-0.290	-4.537	1.00	19.55
6320	OWO	WAT	W	107	29.643	15.604	46.570	1.00	15.52	6365	OWO	WAT	W	152	69.349	10.471	29.638	1.00	25.61
6321	OWO	WAT	W	108	77.037	-3.080	44.844	1.00	17.45	6366	OWO	WAT	W	153	75.556	-7.180	31.034	1.00	17.73
6322	OWO	WAT	W	109	71.489	-9.613	39.434	1.00	14.35	6367	OWO	WAT	W	154	77.494	-24.179	15.886	1.00	19.43
6323	OWO	WAT	W	110	41.593	-4.442	45.963	1.00	18.94	6368	OWO	WAT	W	155	62.259	12.967	49.436	1.00	16.99
6324	OWO	WAT	W	111	63.736	-11.016	10.939	1.00	17.44	6369	OWO	WAT	W	157	81.536	-10.806	5.685	1.00	17.76
6325	OWO	WAT	W	112	40.024	2.255	37.806	1.00	13.52	6370	OWO	WAT	W	158	62.854	-16.944	21.280	1.00	30.32
6326	OWO	WAT	W	113	64.610	-1.339	34.837	1.00	14.96	6371	OWO	WAT	W	159	47.815	-3.762	20.195	1.00	24.16
6327	OWO	WAT	W	114	61.987	20.548	50.028	1.00	19.83	6372	OWO	WAT	W	160	74.332	-2.627	26.574	1.00	20.89
6328	OWO	WAT	W	115	72.528	-7.124	29.593	1.00	18.15	6373	OWO	WAT	W	161	73.134	-8.343	11.701	1.00	14.37
6329	OWO	WAT	W	116	47.271	-11.141	34.789	1.00	18.03	6374	OWO	WAT	W	162	35.562	-10.370	30.256	1.00	16.76
6330	OWO	WAT	W	117	50.553	17.125	41.460	1.00	18.99	6375	OWO	WAT	W	163	89.451	-13.445	20.007	1.00	17.74
6331	OWO	WAT	W	118	54.956	14.273	35.671	1.00	17.04	6376	OWO	WAT	W	164	64.437	-8.353	11.350	1.00	19.87
6332	OWO	WAT	W	119	22.721	16.885	49.692	1.00	18.22	6377	OWO	WAT	W	165	42.448	-1.014	52.692	1.00	25.22
6333	OWO	WAT	W	120	68.820	9.178	39.628	1.00	15.40	6378	OWO	WAT	W	166	46.191	-7.466	32.597	1.00	19.58
6334	OWO	WAT	W	121	58.258	13.263	29.566	1.00	17.29	6379	OWO	WAT	W	167	74.558	-4.139	51.689	1.00	21.48
6335	OWO	WAT	W	122	51.860	-6.953	40.625	1.00	16.39	6380	OWO	WAT	W	168	58.355	12.098	38.036	1.00	18.33
6336	OWO	WAT	W	123	24.503	9.804	33.921	1.00	16.52	6381	OWO	WAT	W	169	64.827	20.010	32.662	1.00	24.95
6337	OWO	WAT	W	124	82.641	-4.698	41.936	1.00	23.28	6382	OWO	WAT	W	170	46.993	18.543	20.841	1.00	20.41
6338	OWO	WAT	W	125	81.955	-8.160	8.351	1.00	24.39	6383	OWO	WAT	W	171	35.631	21.698	36.640	1.00	16.68
6339	OWO	WAT	W	126	62.535	5.308	26.770	1.00	21.48	6384	OWO	WAT	W	172	54.527	4.577	34.040	1.00	16.16
6340	OWO	WAT	W	127	46.588	-10.586	39.440	1.00	17.61	6385	OWO	WAT	W	173	79.048	-13.312	16.275	1.00	19.28

6386	OWO WAT W 174	34.755	5.781	57.522	1.00 28.62	6431	OWO WAT W 220	75.425	-5.678	28.718	1.00 14.44
6387	OWO WAT W 175	24.290	-8.263	41.358	1.00 27.30	6432	OWO WAT W 221	64.613	5.872	48.455	1.00 15.74
6388	OWO WAT W 176	43.005	20.391	32.602	1.00 20.84	6433	OWO WAT W 222	76.468	4.175	45.089	1.00 15.34
6389	OWO WAT W 177	30.870	-2.649	54.736	1.00 25.48	6434	OWO WAT W 223	78.530	-3.248	30.018	1.00 18.35
6390	OWO WAT W 178	53.261	8.959	50.601	1.00 24.03	6435	OWO WAT W 224	66.447	-15.601	45.227	1.00 21.57
6391	OWO WAT W 179	53.517	5.558	31.784	1.00 24.92	6436	OWO WAT W 225	64.601	13.864	43.344	1.00 19.79
6392	OWO WAT W 180	68.153	-15.586	16.468	1.00 17.73	6437	OWO WAT W 226	84.129	-21.451	40.447	1.00 23.07
6393	OWO WAT W 181	80.333	-14.549	-8.414	1.00 28.75	6438	OWO WAT W 227	50.240	9.246	25.360	1.00 27.34
6394	OWO WAT W 182	77.155	4.046	42.470	1.00 16.63	6439	OWO WAT W 228	71.340	-3.838	2.003	1.00 28.41
6395	OWO WAT W 183	36.194	17.220	43.863	1.00 17.32	6440	OWO WAT W 229	85.282	-20.669	0.886	1.00 31.69
6396	OWO WAT W 184	74.883	3.842	36.360	1.00 18.34	6441	OWO WAT W 230	26.568	-10.850	46.117	1.00 21.74
6397	OWO WAT W 185	43.383	31.022	45.350	1.00 34.65	6442	OWO WAT W 231	70.878	-18.207	31.358	1.00 23.68
6398	OWO WAT W 186	55.792	6.996	60.761	1.00 19.70	6443	OWO WAT W 232	35.309	24.294	36.012	1.00 20.39
6399	OWO WAT W 187	62.221	10.100	60.967	1.00 17.41	6444	OWO WAT W 233	52.580	4.977	18.388	1.00 22.44
6400	OWO WAT W 188	72.467	-14.137	23.905	1.00 18.11	6445	OWO WAT W 234	50.557	11.295	58.608	1.00 20.04
6401	OWO WAT W 189	43.775	-10.296	29.108	1.00 13.72	6446	OWO WAT W 235	23.949	20.846	34.191	1.00 26.29
6402	OWO WAT W 190	46.321	8.776	37.734	1.00 17.82	6447	OWO WAT W 236	35.623	14.411	43.636	1.00 19.95
6403	OWO WAT W 191	58.197	4.756	57.467	1.00 18.48	6448	OWO WAT W 237	64.405	-7.438	8.777	1.00 24.16
6404	OWO WAT W 192	18.946	19.472	50.053	1.00 43.73	6449	OWO WAT W 238	75.075	-15.366	34.214	1.00 24.35
6405	OWO WAT W 193	46.641	23.645	40.314	1.00 15.11	6450	OWO WAT W 239	49.008	-14.858	26.445	1.00 18.45
6406	OWO WAT W 194	73.073	2.447	2.145	1.00 25.40	6451	OWO WAT W 240	67.130	18.121	47.777	1.00 26.38
6407	OWO WAT W 195	69.006	20.130	42.674	1.00 23.03	6452	OWO WAT W 241	58.462	-8.275	-6.771	1.00 27.46
6408	OWO WAT W 196	68.843	-18.109	15.825	1.00 22.65	6453	OWO WAT W 242	89.032	-3.538	32.201	1.00 37.77
6409	OWO WAT W 197	18.045	9.415	37.687	1.00 23.22	6454	OWO WAT W 243	76.413	-9.886	12.043	1.00 19.59
6410	OWO WAT W 198	19.821	3.539	53.564	1.00 25.47	6455	OWO WAT W 244	91.058	-23.122	27.002	1.00 29.55
6411	OWO WAT W 199	37.934	-8.358	42.258	1.00 22.96	6456	OWO WAT W 245	68.897	-16.420	32.353	1.00 17.73
6412	OWO WAT W 200	66.324	-17.028	33.133	1.00 21.67	6457	OWO WAT W 246	60.787	20.118	45.579	1.00 19.06
6413	OWO WAT W 201	89.568	-0.730	43.526	1.00 39.85	6458	OWO WAT W 247	57.295	9.602	38.862	1.00 18.19
6414	OWO WAT W 202	65.791	-8.953	56.239	1.00 24.77	6459	OWO WAT W 248	51.834	13.502	33.252	1.00 16.33
6415	OWO WAT W 203	30.336	-3.688	-15.714	1.00 31.23	6460	OWO WAT W 250	37.078	29.140	45.806	1.00 19.44
6416	OWO WAT W 204	38.412	2.069	31.675	1.00 14.46	6461	OWO WAT W 251	79.365	-4.623	6.311	1.00 27.30
6417	OWO WAT W 205	48.840	-16.134	30.302	1.00 22.40	6462	OWO WAT W 252	50.994	3.684	58.665	1.00 26.14
6418	OWO WAT W 206	66.776	20.286	40.341	1.00 25.65	6463	OWO WAT W 253	16.237	1.326	45.058	1.00 21.57
6419	OWO WAT W 207	37.823	3.881	27.553	1.00 16.42	6464	OWO WAT W 254	59.347	18.360	43.822	1.00 21.00
6420	OWO WAT W 208	51.918	25.040	45.285	1.00 35.74	6465	OWO WAT W 255	93.718	-8.612	37.885	1.00 27.72
6421	OWO WAT W 209	57.850	21.185	46.630	1.00 23.05	6466	OWO WAT W 256	18.476	13.116	37.804	1.00 20.53
6422	OWO WAT W 210	20.044	17.034	49.140	1.00 14.24	6467	OWO WAT W 257	74.988	-1.264	7.841	1.00 23.15
6423	OWO WAT W 211	71.715	-5.894	10.737	1.00 16.38	6468	OWO WAT W 258	65.708	-9.485	2.882	1.00 24.47
6424	OWO WAT W 212	66.725	-5.950	11.424	1.00 25.24	6469	OWO WAT W 259	81.228	-18.556	15.613	1.00 21.70
6425	OWO WAT W 213	69.977	-19.080	28.620	1.00 22.47	6470	OWO WAT W 260	40.153	18.506	50.014	1.00 29.11
6426	OWO WAT W 214	41.220	-1.629	45.498	1.00 14.57	6471	OWO WAT W 261	76.275	-15.000	27.216	1.00 14.07
6427	OWO WAT W 215	80.849	-10.168	9.676	1.00 15.11	6472	OWO WAT W 262	32.653	-11.672	30.238	1.00 24.10
6428	OWO WAT W 216	55.460	-4.423	5.582	1.00 25.44	6473	OWO WAT W 263	33.719	19.637	32.612	1.00 23.35
6429	OWO WAT W 217	60.371	3.984	54.712	1.00 19.11	6474	OWO WAT W 264	57.975	6.308	29.825	1.00 28.17
6430	OWO WAT W 218	46.146	-14.480	-19.119	1.00 22.68	6475	OWO WAT W 265	56.014	3.037	13.415	1.00 27.45

6476	OWO	WAT	W 266	35.289	-10.133	-21.987	1.00	24.36	6521	OWO	WAT	W 311	37.738	11.900	54.333	1.00	30.73
6477	OWO	WAT	W 267	48.772	-1.478	-18.710	1.00	22.08	6522	OWO	WAT	W 312	78.463	-14.147	-10.311	1.00	23.91
6478	OWO	WAT	W 268	56.907	-15.816	-21.447	1.00	21.69	6523	OWO	WAT	W 313	46.583	-15.364	34.986	1.00	23.46
6479	OWO	WAT	W 269	70.103	-9.623	56.538	1.00	21.05	6524	OWO	WAT	W 314	62.766	5.097	12.438	1.00	22.65
6480	OWO	WAT	W 270	66.182	8.595	31.274	1.00	23.04	6525	OWO	WAT	W 315	43.230	0.820	-21.984	1.00	35.81
6481	OWO	WAT	W 271	43.509	-7.089	-19.497	1.00	25.51	6526	OWO	WAT	W 316	43.950	4.358	-15.650	1.00	23.67
6482	OWO	WAT	W 272	75.559	-23.596	13.036	1.00	25.28	6527	OWO	WAT	W 317	42.859	-10.546	45.639	1.00	32.28
6483	OWO	WAT	W 273	52.581	11.622	50.505	1.00	19.81	6528	OWO	WAT	W 318	49.162	-3.978	1.765	1.00	43.38
6484	OWO	WAT	W 274	70.407	-23.742	7.358	1.00	26.46	6529	OWO	WAT	W 319	60.903	21.253	54.960	1.00	32.40
6485	OWO	WAT	W 275	47.060	18.265	28.697	1.00	32.17	6530	OWO	WAT	W 320	84.179	-7.984	18.419	1.00	21.93
6486	OWO	WAT	W 276	45.135	20.614	54.168	1.00	26.24	6531	OWO	WAT	W 321	44.701	-15.753	-5.792	1.00	24.15
6487	OWO	WAT	W 277	78.588	-20.221	12.456	1.00	28.74	6532	OWO	WAT	W 322	17.649	6.695	35.037	1.00	33.00
6488	OWO	WAT	W 278	26.272	-3.352	44.999	1.00	18.45	6533	OWO	WAT	W 323	39.424	-10.529	42.109	1.00	24.43
6489	OWO	WAT	W 279	27.844	23.521	45.472	1.00	19.15	6534	OWO	WAT	W 324	17.053	-3.033	44.924	1.00	32.20
6490	OWO	WAT	W 280	43.415	-9.483	-20.814	1.00	21.62	6535	OWO	WAT	W 325	71.659	-19.394	34.189	1.00	29.67
6491	OWO	WAT	W 281	44.928	-9.823	21.085	1.00	21.62	6536	OWO	WAT	W 326	60.464	-11.885	54.688	1.00	29.00
6492	OWO	WAT	W 282	67.718	4.640	5.963	1.00	25.19	6537	OWO	WAT	W 327	60.150	8.501	29.954	1.00	22.12
6493	OWO	WAT	W 283	96.982	-10.458	37.245	1.00	30.81	6538	OWO	WAT	W 328	71.908	12.459	33.945	1.00	31.00
6494	OWO	WAT	W 284	48.457	4.929	-7.033	1.00	23.97	6539	OWO	WAT	W 329	50.518	-6.710	-4.970	1.00	24.35
6495	OWO	WAT	W 285	55.985	-7.377	-3.129	1.00	27.03	6540	OWO	WAT	W 330	81.378	-2.927	27.039	1.00	28.44
6496	OWO	WAT	W 286	35.786	-2.048	0.183	1.00	30.57	6541	OWO	WAT	W 331	69.282	-16.298	45.601	1.00	27.45
6497	OWO	WAT	W 287	78.219	-5.390	40.921	1.00	16.49	6542	OWO	WAT	W 332	67.427	-13.423	-6.333	1.00	30.02
6498	OWO	WAT	W 288	77.364	-21.161	31.334	1.00	18.15	6543	OWO	WAT	W 333	46.329	-12.182	37.298	1.00	20.51
6499	OWO	WAT	W 289	50.808	-19.872	31.259	1.00	23.98	6544	OWO	WAT	W 334	48.718	-20.006	-14.082	1.00	29.70
6500	OWO	WAT	W 290	31.863	-12.519	43.355	1.00	21.97	6545	OWO	WAT	W 335	43.754	-13.207	36.811	1.00	26.82
6501	OWO	WAT	W 291	49.112	-1.399	15.411	1.00	32.14	6546	OWO	WAT	W 336	64.098	14.236	26.166	1.00	29.05
6502	OWO	WAT	W 292	36.747	2.739	53.684	1.00	28.77	6547	OWO	WAT	W 337	37.049	3.266	-19.372	1.00	31.08
6503	OWO	WAT	W 293	47.932	-3.952	50.396	1.00	29.44	6548	OWO	WAT	W 338	61.795	-10.158	-4.790	1.00	34.78
6504	OWO	WAT	W 294	75.259	-18.091	42.038	1.00	27.99	6549	OWO	WAT	W 339	49.037	0.420	51.729	1.00	23.15
6505	OWO	WAT	W 295	65.026	17.315	32.530	1.00	25.64	6550	OWO	WAT	W 340	75.001	-18.929	4.449	1.00	25.65
6506	OWO	WAT	W 296	78.244	-25.283	12.611	1.00	35.84	6551	OWO	WAT	W 341	65.358	-16.321	0.957	1.00	30.48
6507	OWO	WAT	W 297	85.182	-4.003	27.099	1.00	38.09	6552	OWO	WAT	W 342	42.464	13.861	23.091	1.00	28.92
6508	OWO	WAT	W 298	58.707	-10.508	52.943	1.00	20.88	6553	OWO	WAT	W 343	88.313	-2.838	44.183	1.00	29.50
6509	OWO	WAT	W 299	51.111	17.227	31.022	1.00	29.87	6554	OWO	WAT	W 344	32.606	12.506	24.842	1.00	22.59
6510	OWO	WAT	W 300	61.340	-13.950	17.572	1.00	27.41	6555	OWO	WAT	W 345	56.691	16.693	46.428	1.00	23.81
6511	OWO	WAT	W 301	38.209	-3.845	-22.771	1.00	26.19	6556	OWO	WAT	W 346	91.741	-3.418	41.436	1.00	31.63
6512	OWO	WAT	W 302	72.914	-22.668	6.220	1.00	26.26	6557	OWO	WAT	W 347	41.803	11.235	23.103	1.00	38.16
6513	OWO	WAT	W 303	66.840	-21.476	4.405	1.00	27.43	6558	OWO	WAT	W 348	46.070	-13.919	32.782	1.00	29.90
6514	OWO	WAT	W 304	50.616	-5.935	44.803	1.00	18.59	6559	OWO	WAT	W 349	54.505	-7.501	-20.473	1.00	30.31
6515	OWO	WAT	W 305	77.962	12.398	43.121	1.00	32.94	6560	OWO	WAT	W 350	80.666	-8.291	47.313	1.00	31.98
6516	OWO	WAT	W 306	66.149	-13.682	-12.914	1.00	28.81	6561	OWO	WAT	W 351	72.442	3.961	-1.194	1.00	29.66
6517	OWO	WAT	W 307	82.412	-2.518	2.943	1.00	26.24	6562	OWO	WAT	W 352	37.415	6.655	27.782	1.00	26.05
6518	OWO	WAT	W 308	37.840	23.041	26.322	1.00	28.62	6563	OWO	WAT	W 353	68.123	-17.644	51.248	1.00	32.02
6519	OWO	WAT	W 309	61.723	-12.439	11.952	1.00	27.68	6564	OWO	WAT	W 354	61.089	23.461	40.340	1.00	27.24
6520	OWO	WAT	W 310	45.805	-15.302	29.600	1.00	42.22	6565	OWO	WAT	W 355	19.026	-6.909	51.121	1.00	26.68

6746	OWO	WAT	W	538	79.423	-0.659	26.417	1.00	32.62	6791	OWO	WAT	W	583	64.653	-13.766	4.879	1.00	38.84
6747	OWO	WAT	W	539	27.499	-9.225	41.241	1.00	38.84	6792	OWO	WAT	W	584	46.486	-2.333	51.867	1.00	65.57
6748	OWO	WAT	W	540	38.460	-17.144	-22.854	1.00	32.97	6793	OWO	WAT	W	585	76.557	6.773	47.617	1.00	30.66
6749	OWO	WAT	W	541	95.109	-18.447	21.117	1.00	45.20	6794	OWO	WAT	W	586	55.689	0.519	60.810	1.00	37.55
6750	OWO	WAT	W	542	46.885	1.862	-21.845	1.00	45.25	6795	OWO	WAT	W	587	77.597	-7.073	50.855	1.00	34.75
6751	OWO	WAT	W	543	72.300	15.489	37.082	1.00	38.81	6796	OWO	WAT	W	588	88.395	-13.032	11.580	1.00	29.59
6752	OWO	WAT	W	544	53.484	-19.303	24.437	1.00	31.94	6797	OWO	WAT	W	589	41.920	18.111	24.362	1.00	32.25
6753	OWO	WAT	W	545	68.271	-16.075	53.457	1.00	33.31	6798	OWO	WAT	W	590	37.249	-12.482	31.297	1.00	28.69
6754	OWO	WAT	W	546	81.187	-12.562	8.492	1.00	31.48	6799	OWO	WAT	W	591	82.022	-21.727	0.851	1.00	41.41
6755	OWO	WAT	W	547	49.103	-15.891	43.116	1.00	33.62	6800	OWO	WAT	W	592	74.315	9.720	29.056	1.00	36.96
6756	OWO	WAT	W	548	63.252	-20.894	18.880	1.00	38.97	6801	OWO	WAT	W	593	53.410	5.026	-6.751	1.00	40.52
6757	OWO	WAT	W	549	86.032	-2.093	25.031	1.00	38.83	6802	OWO	WAT	W	594	47.536	10.717	59.474	1.00	44.35
6758	OWO	WAT	W	550	50.812	-9.332	-2.366	1.00	32.70	6803	OWO	WAT	W	595	53.540	-15.820	20.692	1.00	36.01
6759	OWO	WAT	W	551	77.222	-22.310	5.262	1.00	42.02	6804	OWO	WAT	W	596	34.459	-9.657	26.624	1.00	33.62
6760	OWO	WAT	W	552	87.105	0.417	40.246	1.00	33.75	6805	OWO	WAT	W	597	67.159	18.723	29.650	1.00	47.65
6761	OWO	WAT	W	553	39.779	-10.913	28.103	1.00	32.23	6806	OWO	WAT	W	598	57.902	-6.416	11.043	1.00	36.87
6762	OWO	WAT	W	554	80.530	5.700	44.684	1.00	22.37	6807	OWO	WAT	W	599	33.150	10.072	56.599	1.00	36.61
6763	OWO	WAT	W	555	44.445	21.933	51.741	1.00	40.68	6808	OWO	WAT	W	600	80.247	-13.720	45.923	1.00	38.71
6764	OWO	WAT	W	556	78.037	4.895	33.580	1.00	38.94	6809	OWO	WAT	W	601	65.256	5.486	60.044	1.00	25.49
6765	OWO	WAT	W	557	50.785	-1.091	53.731	1.00	40.29	6810	OWO	WAT	W	602	70.764	-21.357	-4.897	1.00	34.79
6766	OWO	WAT	W	558	48.427	-18.608	31.494	1.00	38.93	6811	OWO	WAT	W	603	43.485	-13.298	22.439	1.00	36.93
6767	OWO	WAT	W	559	36.861	8.729	55.912	1.00	32.41	6812	OWO	WAT	W	604	55.370	23.838	31.451	1.00	40.61
6768	OWO	WAT	W	560	34.764	8.292	57.897	1.00	41.50	6813	OWO	WAT	W	605	72.230	-4.477	53.756	1.00	33.63
6769	OWO	WAT	W	561	52.719	-18.428	-15.193	1.00	34.83	6814	OWO	WAT	W	606	86.015	-6.308	44.482	1.00	33.31
6770	OWO	WAT	W	562	21.141	21.506	43.413	1.00	35.68	6815	OWO	WAT	W	607	79.100	6.742	28.261	1.00	39.66
6771	OWO	WAT	W	563	32.675	10.931	22.641	1.00	33.70	6816	OWO	WAT	W	608	13.024	10.093	41.592	1.00	39.66
6772	OWO	WAT	W	564	79.498	-28.457	28.133	1.00	41.72	6817	OWO	WAT	W	610	19.065	2.738	56.666	1.00	36.22
6773	OWO	WAT	W	565	31.047	-13.425	34.555	1.00	32.76	6818	OWO	WAT	W	611	27.698	18.474	28.229	1.00	29.78
6774	OWO	WAT	W	566	17.333	-4.663	51.771	1.00	23.15	6819	OWO	WAT	W	612	79.524	-22.037	-5.261	1.00	35.00
6775	OWO	WAT	W	567	73.981	-25.793	-1.995	1.00	46.66	6820	OWO	WAT	W	613	78.777	3.843	-0.369	1.00	39.60
6776	OWO	WAT	W	568	54.933	7.887	31.452	1.00	35.09	6821	OWO	WAT	W	614	60.674	23.492	32.021	1.00	50.31
6777	OWO	WAT	W	569	40.812	-13.172	37.899	1.00	34.36	6822	OWO	WAT	W	615	89.369	-13.520	6.901	1.00	53.93
6778	OWO	WAT	W	570	90.118	-22.677	43.385	1.00	42.30	6823	OWO	WAT	W	616	54.674	2.066	-7.514	1.00	35.44
6779	OWO	WAT	W	571	49.795	16.333	32.935	1.00	33.34	6824	OWO	WAT	W	617	80.241	-21.114	10.183	1.00	45.60
6780	OWO	WAT	W	572	86.224	-3.103	29.568	1.00	45.18	6825	OWO	WAT	W	618	39.869	-0.368	53.204	1.00	31.86
6781	OWO	WAT	W	573	93.985	-21.593	25.927	1.00	49.38	6826	OWO	WAT	W	619	84.314	0.222	22.029	1.00	38.74
6782	OWO	WAT	W	574	48.711	29.216	31.209	1.00	38.64	6827	OWO	WAT	W	620	77.764	-28.451	25.257	1.00	42.43
6783	OWO	WAT	W	575	80.779	-26.441	29.557	1.00	41.33	6828	OWO	WAT	W	621	92.860	-6.918	29.400	1.00	43.50
6784	OWO	WAT	W	576	30.291	-0.331	-3.469	1.00	33.78	6829	OWO	WAT	W	622	82.066	-22.011	-5.845	1.00	43.27
6785	OWO	WAT	W	577	83.004	-7.012	12.342	1.00	54.12	6830	OWO	WAT	W	624	66.952	21.443	36.324	1.00	35.06
6786	OWO	WAT	W	578	77.402	10.589	36.940	1.00	34.01	6831	OWO	WAT	W	625	65.091	-21.080	25.542	1.00	36.11
6787	OWO	WAT	W	579	36.261	17.002	46.660	1.00	36.83	6832	OWO	WAT	W	626	95.260	-15.509	41.378	1.00	32.64
6788	OWO	WAT	W	580	72.862	13.977	47.223	1.00	31.19	6833	OWO	WAT	W	627	60.917	-1.177	-13.410	1.00	40.04
6789	OWO	WAT	W	581	47.939	-15.885	24.111	1.00	32.81	6834	OWO	WAT	W	628	60.376	-14.353	56.761	1.00	47.88
6790	OWO	WAT	W	582	77.692	9.100	24.255	1.00	39.63	6835	OWO	WAT	W	629	35.528	17.752	-20.354	1.00	38.18

6836	OWO	WAT	W	630	53.084	17.303	25.669	1.00	46.468	6881	OWO	WAT	W	676	21.734	16.509	28.603	1.00	52.662
6837	OWO	WAT	W	631	49.338	24.584	23.434	1.00	37.08	6882	OWO	WAT	W	677	90.154	12.035	4.840	1.00	52.27
6838	OWO	WAT	W	632	44.633	31.369	41.827	1.00	51.68	6883	OWO	WAT	W	678	77.0849	5.083	18.362	1.00	38.43
6839	OWO	WAT	W	633	41.364	9.274	55.363	1.00	48.19	6884	OWO	WAT	W	679	78.809	-3.340	8.660	1.00	44.26
6840	OWO	WAT	W	634	85.480	-8.670	45.623	1.00	38.50	6885	OWO	WAT	W	680	37.125	6.546	25.017	1.00	26.76
6841	OWO	WAT	W	635	67.366	8.090	27.660	1.00	46.28	6886	OWO	WAT	W	681	65.476	13.560	57.511	1.00	38.57
6842	OWO	WAT	W	636	58.044	20.208	61.858	1.00	40.81	6887	OWO	WAT	W	682	54.416	3.948	15.578	1.00	40.81
6843	OWO	WAT	W	637	60.247	-6.665	-19.077	1.00	33.84	6888	OWO	WAT	W	683	53.062	-18.088	22.008	1.00	43.119
6844	OWO	WAT	W	638	22.729	2.441	55.615	1.00	38.38	6889	OWO	WAT	W	684	12.292	12.538	42.132	1.00	32.07
6845	OWO	WAT	W	639	58.636	-8.488	-2.049	1.00	45.41	6890	OWO	WAT	W	685	22.886	9.102	31.205	1.00	44.59
6846	OWO	WAT	W	640	51.765	-5.454	-24.427	1.00	30.07	6891	OWO	WAT	W	686	24.574	-0.920	55.112	1.00	42.14
6847	OWO	WAT	W	641	60.477	-7.078	-5.334	1.00	51.94	6892	OWO	WAT	W	687	61.965	-4.738	11.865	1.00	34.12
6848	OWO	WAT	W	642	35.217	24.951	48.021	1.00	36.69	6893	OWO	WAT	W	688	54.878	-16.136	18.394	1.00	42.78
6849	OWO	WAT	W	643	25.477	8.964	26.926	1.00	36.50	6894	OWO	WAT	W	689	16.847	19.568	45.126	1.00	43.60
6850	OWO	WAT	W	644	73.038	7.145	25.686	1.00	38.10	6895	OWO	WAT	W	690	55.170	23.039	52.155	1.00	41.75
6851	OWO	WAT	W	645	31.546	26.839	42.458	1.00	37.72	6896	OWO	WAT	W	691	39.834	-12.044	-3.476	1.00	36.25
6852	OWO	WAT	W	646	78.629	5.276	46.680	1.00	30.14	6897	OWO	WAT	W	692	83.900	-19.454	48.185	1.00	42.85
6853	OWO	WAT	W	647	50.352	-10.415	0.030	1.00	34.69	6898	OWO	WAT	W	693	62.276	19.955	30.431	1.00	34.17
6854	OWO	WAT	W	648	32.075	3.622	57.785	1.00	50.55	6899	OWO	WAT	W	694	84.970	-6.738	10.835	1.00	42.23
6855	OWO	WAT	W	649	82.155	-23.495	3.245	1.00	34.51	6900	OWO	WAT	W	695	35.725	-14.462	31.165	1.00	39.86
6856	OWO	WAT	W	650	53.614	-0.820	-5.533	1.00	30.46	6901	OWO	WAT	W	696	58.055	17.975	63.613	1.00	53.19
6857	OWO	WAT	W	651	41.173	6.120	-12.244	1.00	32.87	6902	OWO	WAT	W	697	48.858	27.436	43.339	1.00	47.28
6858	OWO	WAT	W	652	46.461	15.785	29.821	1.00	33.74	6903	OWO	WAT	W	698	63.336	-8.234	57.236	1.00	47.00
6859	OWO	WAT	W	653	46.910	-0.266	53.614	1.00	36.78	6904	OWO	WAT	W	699	70.147	-26.087	29.342	1.00	55.27
6860	OWO	WAT	W	654	54.969	9.457	27.413	1.00	41.28	6905	OWO	WAT	W	700	66.692	-14.096	-16.368	1.00	45.91
6861	OWO	WAT	W	655	71.413	3.244	11.859	1.00	47.81	6906	OWO	WAT	W	701	40.692	15.224	56.764	1.00	46.42
6862	OWO	WAT	W	656	48.713	8.420	-19.259	1.00	36.50	6907	OWO	WAT	W	702	79.719	-28.791	22.760	1.00	32.02
6863	OWO	WAT	W	657	53.539	25.302	32.991	1.00	38.05	6908	OWO	WAT	W	703	59.465	21.759	30.551	1.00	42.42
6864	OWO	WAT	W	658	53.590	-1.475	8.457	1.00	51.45	6909	OWO	WAT	W	704	31.141	-5.131	22.552	1.00	68.52
6865	OWO	WAT	W	659	79.662	-22.479	-0.183	1.00	50.01	6910	OWO	WAT	W	705	36.695	-16.973	-4.878	1.00	37.89
6866	OWO	WAT	W	660	18.141	15.650	34.789	1.00	53.01	6911	OWO	WAT	W	706	80.687	-20.765	47.288	1.00	38.30
6867	OWO	WAT	W	661	87.154	-0.180	42.783	1.00	47.33	6912	OWO	WAT	W	707	54.669	3.010	-9.815	1.00	46.05
6868	OWO	WAT	W	662	62.459	9.375	29.050	1.00	30.93	6913	OWO	WAT	W	708	43.216	-8.260	47.123	1.00	40.03
6869	OWO	WAT	W	663	42.984	25.814	49.065	1.00	34.72	6914	OWO	WAT	W	709	70.862	15.600	41.973	1.00	37.00
6870	OWO	WAT	W	664	89.832	-5.536	43.041	1.00	35.89	6915	OWO	WAT	W	710	33.412	-2.522	54.114	1.00	48.11
6871	OWO	WAT	W	666	95.356	-6.463	30.956	1.00	39.83	6916	OWO	WAT	W	711	92.535	-0.923	34.738	1.00	49.47
6872	OWO	WAT	W	667	70.567	14.899	27.721	1.00	47.74	6917	OWO	WAT	W	712	33.025	23.917	47.317	1.00	46.24
6873	OWO	WAT	W	668	38.060	1.861	56.019	1.00	43.81	6918	OWO	WAT	W	713	70.249	17.850	37.204	1.00	40.78
6874	OWO	WAT	W	669	42.573	-12.553	29.782	1.00	44.56	6919	OWO	WAT	W	714	41.368	22.495	53.675	1.00	40.32
6875	OWO	WAT	W	670	63.052	-18.013	29.178	1.00	32.11	6920	OWO	WAT	W	715	76.578	-19.899	49.657	1.00	40.87
6876	OWO	WAT	W	671	26.904	-12.528	-19.449	1.00	50.32	6921	OWO	WAT	W	716	90.425	-4.420	30.203	1.00	60.30
6877	OWO	WAT	W	672	87.381	-14.602	9.308	1.00	38.68	6922	OWO	WAT	W	717	34.487	19.062	20.833	1.00	45.89
6878	OWO	WAT	W	673	73.626	-6.763	27.221	1.00	44.79	6923	OWO	WAT	W	718	89.801	-4.016	22.869	1.00	46.61
6879	OWO	WAT	W	674	19.297	10.427	29.648	1.00	53.79	6924	OWO	WAT	W	719	74.377	1.047	-13.486	1.00	51.80
6880	OWO	WAT	W	675	61.974	-17.776	43.690	1.00	45.64	6925	OWO	WAT	W	720	66.043	9.718	1.00	41.97	

6926	OWO	WAT	W	721	56.444	-17.979	-12.402	1.00	40.83	6971	OWO	WAT	W	766	84.664	-22.555	14.359	1.00	45.78
6927	OWO	WAT	W	722	82.588	-0.182	1.654	1.00	55.22	6972	OWO	WAT	W	767	30.072	-20.212	-10.959	1.00	38.35
6928	OWO	WAT	W	723	61.949	-0.825	-0.993	1.00	44.85	6973	OWO	WAT	W	768	41.072	-0.946	-21.837	1.00	41.66
6929	OWO	WAT	W	724	91.665	-3.882	41.279	1.00	43.45	6974	OWO	WAT	W	769	61.874	11.916	27.798	1.00	44.81
6930	OWO	WAT	W	725	78.637	-22.418	46.944	1.00	49.42	6975	OWO	WAT	W	770	66.356	5.178	-1.773	1.00	65.15
6931	OWO	WAT	W	726	76.801	0.776	11.150	1.00	43.15	6976	OWO	WAT	W	771	26.844	5.186	59.968	1.00	46.27
6932	OWO	WAT	W	727	36.682	26.179	34.703	1.00	40.16	6977	OWO	WAT	W	772	36.878	24.305	28.318	1.00	34.70
6933	OWO	WAT	W	728	52.946	-24.152	35.886	1.00	42.32	6978	OWO	WAT	W	773	54.912	-1.550	-21.819	1.00	42.64
6934	OWO	WAT	W	729	44.065	-10.820	0.741	1.00	58.49	6979	OWO	WAT	W	774	59.594	-17.858	41.366	1.00	37.27
6935	OWO	WAT	W	730	59.442	-15.580	42.690	1.00	31.69	6980	OWO	WAT	W	775	57.520	-15.150	18.294	1.00	36.30
6936	OWO	WAT	W	731	72.384	8.537	51.566	1.00	31.82	6981	OWO	WAT	W	776	32.998	24.523	34.324	1.00	42.23
6937	OWO	WAT	W	732	31.347	-6.053	26.265	1.00	42.64	6982	OWO	WAT	W	777	59.020	-12.114	56.789	1.00	57.61
6938	OWO	WAT	W	733	34.630	6.679	23.929	1.00	43.41	6983	OWO	WAT	W	778	81.113	-27.278	43.621	1.00	41.79
6939	OWO	WAT	W	734	57.088	-11.759	-15.829	1.00	40.44	6984	OWO	WAT	W	779	73.319	-20.756	38.654	1.00	43.17
6940	OWO	WAT	W	735	79.179	-22.870	6.833	1.00	45.12	6985	OWO	WAT	W	780	75.478	-16.566	37.845	1.00	51.42
6941	OWO	WAT	W	736	38.310	-14.037	35.139	1.00	44.86	6986	OWO	WAT	W	781	91.610	-6.042	15.770	1.00	36.38
6942	OWO	WAT	W	737	39.171	-2.907	53.911	1.00	45.60	6987	OWO	WAT	W	782	71.605	16.644	39.410	1.00	48.62
6943	OWO	WAT	W	738	39.322	17.927	28.434	1.00	40.22	6988	OWO	WAT	W	783	63.508	24.207	41.029	1.00	44.22
6944	OWO	WAT	W	739	48.359	2.635	58.769	1.00	51.66	6989	OWO	WAT	W	784	88.822	-11.109	7.822	1.00	48.78
6945	OWO	WAT	W	740	72.823	5.269	52.825	1.00	45.87	6990	OWO	WAT	W	785	71.691	-23.906	33.801	1.00	48.29
6946	OWO	WAT	W	741	52.762	19.727	28.434	1.00	40.22	6991	OWO	WAT	W	786	52.032	8.913	29.301	1.00	39.41
6947	OWO	WAT	W	742	28.202	-5.793	-6.513	1.00	48.77	6992	OWO	WAT	W	787	72.141	14.023	31.846	1.00	37.55
6948	OWO	WAT	W	743	79.618	1.235	4.432	1.00	42.94	6993	OWO	WAT	W	788	39.138	16.149	26.862	1.00	50.27
6949	OWO	WAT	W	744	67.094	-18.257	47.501	1.00	38.02	6994	OWO	WAT	W	789	37.813	-9.039	47.875	1.00	13.18
6950	OWO	WAT	W	745	52.688	10.357	62.956	1.00	40.29	6995	OWO	WAT	W	790	35.173	-8.363	50.198	1.00	39.87
6951	OWO	WAT	W	746	40.431	-14.509	-4.481	1.00	42.77	6996	OWO	WAT	W	791	26.847	-1.258	31.548	1.00	39.21
6952	OWO	WAT	W	747	38.750	-10.992	22.885	1.00	44.88	6997	OWO	WAT	W	792	88.614	-23.766	1.624	1.00	50.125
6953	OWO	WAT	W	748	44.292	14.402	59.454	1.00	44.70	6998	OWO	WAT	W	793	21.121	7.089	31.169	1.00	50.12
6954	OWO	WAT	W	749	56.054	-11.968	53.046	1.00	41.34	6999	OWO	WAT	W	794	41.636	21.622	50.969	1.00	47.76
6955	OWO	WAT	W	750	44.966	-16.181	23.899	1.00	50.48	7000	OWO	WAT	W	795	26.421	0.362	29.613	1.00	43.60
6956	OWO	WAT	W	751	41.969	29.748	47.846	1.00	20.30	7001	OWO	WAT	W	796	44.401	-8.843	-23.747	1.00	40.62
6957	OWO	WAT	W	752	44.966	-16.181	23.899	1.00	50.48	7002	OWO	WAT	W	797	70.057	18.053	42.138	1.00	38.55
6958	OWO	WAT	W	753	85.694	-22.932	2.568	1.00	43.55	7003	OWO	WAT	W	798	66.270	-17.604	-6.916	1.00	45.58
6959	OWO	WAT	W	754	43.034	6.314	-21.514	1.00	51.86	7004	OWO	WAT	W	799	45.167	31.367	45.147	1.00	51.35
6960	OWO	WAT	W	755	84.872	4.181	42.842	1.00	49.44	7005	OWO	WAT	W	800	75.137	5.508	51.679	1.00	45.47
6961	OWO	WAT	W	756	74.363	11.696	34.959	1.00	37.97	7006	OWO	WAT	W	801	18.046	3.941	59.147	1.00	42.23
6962	OWO	WAT	W	757	80.803	5.977	33.052	1.00	43.92	7007	OWO	WAT	W	802	59.339	0.402	-2.076	1.00	52.88
6963	OWO	WAT	W	758	61.280	17.301	58.888	1.00	40.96	7008	OWO	WAT	W	803	55.564	-18.287	-15.179	1.00	38.85
6964	OWO	WAT	W	759	35.859	19.793	23.282	1.00	48.10	7009	OWO	WAT	W	804	28.418	0.009	26.267	1.00	52.59
6965	OWO	WAT	W	760	25.248	19.237	32.614	1.00	31.76	7010	OWO	WAT	W	805	97.132	-12.269	27.826	1.00	38.21
6966	OWO	WAT	W	761	10.189	11.762	36.214	1.00	43.45	7011	OWO	WAT	W	806	21.485	21.769	33.106	1.00	37.24
6967	OWO	WAT	W	762	46.595	-5.917	-22.133	1.00	44.31	7012	OWO	WAT	W	807	61.494	-16.277	-11.458	1.00	32.92
6968	OWO	WAT	W	763	20.413	11.283	60.057	1.00	50.11	7013	OWO	WAT	W	808	77.944	0.149	8.828	1.00	56.65
6969	OWO	WAT	W	764	68.167	5.712	13.653	1.00	30.67	7014	OWO	WAT	W	809	75.983	-17.170	-12.760	1.00	45.38
6970	OWO	WAT	W	765	54.184	2.615	-12.252	1.00	39.38	7015	OWO	WAT	W	810	52.665	-11.955	-2.121	1.00	42.83

7016	OWO WAT W 811	54.291	-1.443	-1.785	1.00 38.65	7061	OWO WAT W 856	23.937	14.064	59.101	1.00 46.09
7017	OWO WAT W 812	51.272	6.345	31.812	1.00 46.84	7062	OWO WAT W 857	65.116	20.932	49.254	1.00 41.13
7018	OWO WAT W 813	96.248	-8.528	40.673	1.00 36.47	7063	OWO WAT W 858	38.488	17.732	55.214	1.00 40.12
7019	OWO WAT W 814	21.883	-7.783	54.051	1.00 37.11	7064	OWO WAT W 859	39.060	7.114	-23.052	1.00 31.07
7020	OWO WAT W 815	41.687	30.174	33.806	1.00 43.95	7065	OWO WAT W 860	44.261	9.954	-10.440	1.00 45.44
7021	OWO WAT W 816	49.364	-19.438	-8.102	1.00 46.98	7066	OWO WAT W 861	57.678	24.011	45.961	1.00 35.78
7022	OWO WAT W 817	63.992	20.309	53.102	1.00 38.77	7067	OWO WAT W 862	62.731	-18.645	24.010	1.00 34.48
7023	OWO WAT W 818	65.323	12.002	26.726	1.00 45.31	7068	OWO WAT W 863	55.872	23.413	49.005	1.00 52.80
7024	OWO WAT W 819	44.245	-15.998	36.333	1.00 36.72	7069	OWO WAT W 864	78.578	2.825	2.653	1.00 47.81
7025	OWO WAT W 820	61.512	-12.703	-20.772	1.00 42.86	7070	OWO WAT W 865	82.130	-6.162	9.951	1.00 45.86
7026	OWO WAT W 821	40.874	-3.535	-22.568	1.00 37.17	7071	OWO WAT W 866	69.803	-18.155	38.558	1.00 50.20
7027	OWO WAT W 822	53.950	22.361	28.394	1.00 48.45	7072	OWO WAT W 867	11.916	7.726	43.912	1.00 34.68
7028	OWO WAT W 823	47.488	6.176	-13.884	1.00 39.21			11.916	7.726	43.912	1.00 34.68
7029	OWO WAT W 824	62.078	-1.860	61.143	1.00 48.06						
7030	OWO WAT W 825	83.442	-26.335	2.633	1.00 59.67						
7031	OWO WAT W 826	82.792	-0.371	24.014	1.00 41.82						
7032	OWO WAT W 827	49.672	12.353	60.988	1.00 43.87						
7033	OWO WAT W 828	41.022	-7.720	48.703	1.00 39.62						
7034	OWO WAT W 829	64.480	1.533	-6.989	1.00 39.53						
7035	OWO WAT W 830	19.350	12.831	57.326	1.00 35.73						
7036	OWO WAT W 831	22.229	14.191	30.825	1.00 54.08						
7037	OWO WAT W 832	69.924	16.102	52.996	1.00 35.01						
7038	OWO WAT W 833	80.371	-18.513	48.901	1.00 45.56						
7039	OWO WAT W 834	64.966	-13.780	2.163	1.00 45.15						
7040	OWO WAT W 835	90.651	-7.000	22.378	1.00 39.28						
7041	OWO WAT W 836	70.311	5.553	14.709	1.00 31.82						
7042	OWO WAT W 837	45.088	24.790	51.597	1.00 50.96						
7043	OWO WAT W 838	65.259	23.437	36.483	1.00 58.46						
7044	OWO WAT W 839	23.969	-18.104	-13.469	1.00 44.45						
7045	OWO WAT W 840	98.275	-11.384	39.798	1.00 40.16						
7046	OWO WAT W 841	43.468	-4.550	50.159	1.00 42.27						
7047	OWO WAT W 842	55.531	24.997	41.758	1.00 43.49						
7048	OWO WAT W 843	79.423	-25.689	-0.377	1.00 50.83						
7049	OWO WAT W 844	82.729	-5.447	14.530	1.00 37.55						
7050	OWO WAT W 845	57.277	-20.688	32.754	1.00 27.47						
7051	OWO WAT W 846	34.927	18.980	47.765	1.00 43.87						
7052	OWO WAT W 847	66.697	21.490	33.750	1.00 55.52						
7053	OWO WAT W 848	52.866	-18.940	42.635	1.00 48.02						
7054	OWO WAT W 849	50.290	-12.920	19.561	1.00 49.79						
7055	OWO WAT W 850	24.446	5.767	29.203	1.00 39.68						
7056	OWO WAT W 851	44.555	9.373	55.910	1.00 30.53						
7057	OWO WAT W 852	59.190	7.201	65.033	1.00 43.41						
7058	OWO WAT W 853	23.010	7.765	61.451	1.00 52.83						
7059	OWO WAT W 854	22.922	24.189	36.031	1.00 41.20						
7060	OWO WAT W 855	57.790	-3.694	56.332	1.00 51.83						

END

APPENDIX 2

	1				50
Promozyyme	DSTSTKVIVH	YHRFDSNYTN	WDVMMWPYQP	VNGNGAAYQF	TGTNDDPGAV
B.acidopul	DSTSTEVIVH	YHRFDSNYAN	WDLWMWPYQP	VNGNGAAYEF	SG.KDDFGVK
B.deramifi	DGNTTTIIVH	YFRPAGDYQP	WSLWMW...P	KDGGGAEYDF	NQPADSFAGV
	51				100
Promozyyme	ADTQVPGDNT	QVGLIVRKND	WSEKNTPNDL	HIDLAKGHEV	WIVQGDPTIY
B.acidopul	ADVQVPGDDT	QVGLIVRTND	WSQKNTSDDL	HIDLTGHEI	WIVQGDPTIY
B.deramifi	ASADIPGNPS	QVGIIVRTQD	WT.KDVSADR	YIDLSKGNEV	WLVEGNSQIF
	101				150
Promozyyme	YNLSDAQAAA	IPSVSNAYLD	DEKTVLAKLS	MPMTLADAAS	GFTVIDKTTG
B.acidopul	YNLSDAQAAA	TPKVSNAAYLD	NEKTVLAKLT	NPMTLSDGSS	GFTVTDKTTG
B.deramifi	YNEKDAEDAA	KPAVSNAAYLD	ASNQVLVKLS	QPLTLGEGAS	GFTVHDDTAN
	151				197
Promozyyme	EKIPVTSAVS	A...NPVTAV	LVGDLQQALG	AANNWSPDDD	HTLLKKINPN
B.acidopul	EQIPVTAATN	A...NS....
B.deramifi	KDIPVTSVKD	ASLGQDVTAV	LAGTFQHIFG	GS.DWAPDNH	STLLKKVTNN
	198				246
Promozyyme	LYQLSGTLPA	GTQYKIALD	HSW.NTSYPG	NNVSLTVPQG	GEKVTFITYI
B.acidopul
B.deramifi	LYQFSGDLPE	GNQYKVALN	DSWNNPSYPS	DNINLTV PAG	GAHVTFYSYI
	247				296
Promozyyme	STNQVFD SVN	HPNQAFPTSS	AGVQTNLVQL	TLASAPDVTH	NLDVAADGYK
B.acidopulAS	SSEQTDLVQL	TLASAPDVSH	TIQVGAAGYE
B.deramifi	STHAVYDTIN	NPNADLQVES	.GVKTDLVTV	TLGEDPDVSH	TLISIQTGQY
	297				346
Promozyyme	AHNILPRNVL	NLPRYDYSN	DLGNVYSKDA	TSFRVWAPTA	SNVQLLLYNS
B.acidopul	AVNLIPRNVL	NLPRYYSN	DLGNVYSNKA	TAFRVWAPTA	SDVQLLLYNS
B.deramifi	AKQVIPRNVL	NSSQYYSN	DLGNTYTQKA	TTFKVWAPTS	TQVNVLLYDS
	347				396
Promozyyme	EKGSITKQLE	MQKSDNGTWK	LQVSGNLENW	YYLYQVTVNG	TTQTAVDPYA
B.acidopul	ETGPVTKQLE	MQKSDNGTWK	LKVPGNLKNW	YYLYQVTVNG	KTQTAVDPYV
B.deramifi	ATGSVTKIVP	MTASGHGVWE	ATVNQNLENW	YYMYEVTGQG	STRTAVDPYA
	397				446
Promozyyme	RAISVNATRG	MIVDLKATDP	AGWQGDHEQT	PANPVDEVIY	EAHVRDFSID
B.acidopul	RAISVNATRG	MIVDLED TNP	PGWKEDHQQT	PANPVDEVIY	EVHVRDFSID
B.deramifi	TAIAPNGTRG	MIVDLAKTDP	AGWNSDKHIT	PKNIEDEVIY	EMDVRDFSID
	447				496
Promozyyme	ANSGMKNGKG	YLAFTEHGK	GPDHVKTGID	SLKELGITT	QLQPVVEFNS
B.acidopul	ANSGMKNGKG	YLAFTEHGK	GPDNVKTGID	SLKELGINAV	QLQPIEFNS
B.deramifi	PNSGMKNKGK	YLALTEKGK	GPDNVKTGID	SLKQLGITHV	QLMPVFASNS
	497				546
Promozyyme	IDETQPD TYN	WGYDPRNYN	PEGAYATTPE	GTARITELKQ	LIQSLHQQRI
B.acidopul	IDETQPNMYN	WGYDPRNYN	PEGAYATTPE	GTARITQLKQ	LIQSIHKDRI
B.deramifi	VDETDPTQDN	WGYDPRNYDV	PEGQYATNAN	GNARIKEFKE	MVLSLHREHI

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	547				596
Promozyyme	GVNMDVVYNH	TFDVMVSDFD	KIVPQYYYRT	DSNGNYTNGS	GCGNEFATEH
B. acidopul	AINMDVVYNH	TFNVGVSDFD	KIVPQYYYRT	DSAGNYTNGS	GVGNEIATER
B. deramifi	GVNMDVVYNH	TFATQISDFD	KIVPEYYYRT	DDAGNYTNGS	GTGNEIAAER
	597				646
Promozyyme	PMAQKFVLDS	VNYWVNEYHV	DGFRFDLMAL	LGKDTMAKIS	NELHAINPGI
B. acidopul	PMVQKFVLDS	VKYWVKEYHI	DGFRFDLMAL	LGKDTMAKIS	KELHAINPGI
B. deramifi	PMVQKFIIDS	LKYWVNEYHI	DGFRFDLMAL	LGKDTMSKAA	SELHAINPGI
	647				696
Promozyyme	VLYGEPWTGG	TSGLSSDQLV	TKGQQKGLGI	GVFNDNIRNG	LDGNVDFKTA
B. acidopul	VLYGEPWTGG	TSGLSSDQLV	TKGQQKGLGI	GVFNDNIRNG	LDGNVDFKSA
B. deramifi	ALYGEPWTGG	TSALPDDQLL	TKGAQKGMGV	AVFNDNLRNA	LDGNVDFSSA
	697				746
Promozyyme	QGFATGDPNQ	VDVIKNGVIG	SIQDFTSAPS	ETINYVTSHD	NMTLWDKILA
B. acidopul	QGFATGDPNQ	VNVIKNRVMG	SISDFTSAPS	ETINYVTSHD	NMTLWDKISA
B. deramifi	QGFATGATGL	TDAIKNGVEG	SINDFTSSPG	ETINYVTSHD	NYTLWDKIAL
	747				796
Promozyyme	SNPSDTEADR	IKMDELAHAV	VFTSQGVPPM	QGGEEMLRTK	GGNDNSYNAG
B. acidopul	SNPNDTQADR	IKMDELAQAV	VFTSQGVPPM	QGGEEMLRTK	GGNDNSYNAG
B. deramifi	SNPNDSEADR	IKMDELAQAV	VMTSQGVPPM	QGGEEMLRTK	GGNDNSYNAG
	797				846
Promozyyme	DSVNQFDWSR	KAQFKDVPDY	FSSMIHLRNQ	HPAFRMTTAD	QIKQNLTFLE
B. acidopul	DSVNQFDWSR	KAQFENVFDY	YSWLIHLRDN	HPAFRMTTAD	QIKQNLTFLD
B. deramifi	DAVNEFDWSR	KAQYPDVFN Y	YSGLIHLRLD	HPAFRMTTAN	EINSHLQFLN
	847				896
Promozyyme	SPTNTVAFEL	KNYANHDTWK	NIIVMYNPNK	TSQTLNLP SG	DWTIVGLGDQ
B. acidopul	SPTNTVAFEL	KNHANHDKWK	NIIVMYNPNK	TAQTLTLPSG	NWTIVGLGNQ
B. deramifi	SPENTVAYEL	TDHVNKDKWG	NIIVVYNPNK	TVATINLP SG	KWAINATSGK
	897		921		
Promozyyme	IGEKS LGHVM	GNVQVPAIST	LILKQ.....	
B. acidopul	VGEKSLGHVN	GTVEVPALST	IILHQGTSED	VIDQN	
B. deramifi	VGESTLGQAE	GSVQVPGISM	MILHQEVSPD	HGKK.	

5 a) modeling the parent pullulanase on the three-dimensional structure of SEQ
ID NO: 1 depicted in the Appendix to produce a three-dimensional structure
of the parent pullulanase;

10 b) identifying in the three-dimensional structure obtained in step (a) at least
one structural part of the parent pullulanase, wherein an alteration in said
structural part is predicted to result in an altered property;

c) modifying the nucleic acid sequence encoding the parent pullulanase
to produce a nucleic acid sequence encoding a deletion, insertion, or
substitution of one or more amino acids at a position corresponding to said
structural part; and

15 d) expressing the modified nucleic acid sequence in a host cell to produce
the variant pullulanase.

20 3. The method according to claim 2, wherein the altered property is a higher isoamylase activity as defined by an increase of at least 5% in the number of reducing ends formed in the "assay for isoamylase-like activity" described herein, using 50 mM sodium acetate, a pH of 4.5, 5.0 or 5.5, a temperature of 60°C and when incubated with a 10% w/v rabbit liver glycogen solution for a period of 10 min.

25 4. The method according to claims 1 or 2, wherein the altered property is an improved thermostability as defined by differential scanning calorimetry (DSC) using the method described herein.

10. A method for constructing a variant of a parent pullulanase, the method comprising:

- a) identifying an internal or external cavity or crevice in the three-dimensional structure of the parent pullulanase ;
- b) substituting at least one amino acid residue in the neighborhood of the cavity or crevice with another amino acid residue which increases the hydrophobic interaction and/or fills out or reduces the size of the cavity or crevice;
- c) optionally repeating steps a) and b) recursively;
- d) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b);
- e) preparing the variant resulting from steps a) - d);
- f) testing the thermostability of said variant; and
- g) optionally repeating steps a) - f) recursively; and
- h) selecting a variant having increased thermostability as compared to the parent pullulanase.
11. A method for constructing a variant of a parent pullulanase, the method comprising:
- a) identifying in the three-dimensional structure of the parent pullulanase two or more amino acid residues which, when substituted with cysteines, are capable of forming a disulfide bond;
- b) substituting the amino acids identified in a) with cysteines;
- c) optionally repeating steps a) and b) recursively;
- d) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b);
- e) preparing the variant resulting from steps a) - d);

10

- b) substituting, on the surface of the parent pullulanase, at least one amino acid residue selected from the group consisting of Asp, Glu, Arg, Lys and His with an uncharged amino acid residue.

15

- e) preparing the variant resulting from steps a) - d);

- g) optionally repeating steps a) - f) recursively; and

- 20

a) identifying an amino acid sequence which links together two or more domains of the parent pullulanase together;

- b) substituting at least one amino acid residue in the said amino acid sequence with another amino acid residue or deleting at least one amino acid residue in said amino acid sequence;
- c) optionally repeating steps a) and b) recursively;
- 5 d) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b);
- e) preparing the variant resulting from steps a) - d);
- f) testing the thermostability of said variant; and
- g) optionally repeating steps a) - f) recursively; and
- 10 h) selecting a variant having increased thermostability as compared to the parent pullulanase.

14. A method according to claim 13, the method comprising in step b) deleting at least one amino acid residue in said amino acid sequence;

- 15 15. A method according to any of claims 10-14, wherein the increased thermostability is as defined in any of claims 4-9.

16. A method for constructing a variant of a parent pullulanase, where the variant pullulanase has an altered substrate specificity as compared to the parent pullulanase, the method comprising:

- 20 a) identifying the substrate binding area in a model of the three-dimensional structure of the parent pullulanase;
- b) modifying the substrate binding area by an amino acid substitution, deletion and/or insertion;
- c) optionally repeating step b) recursively;

c) optionally repeating steps a) and b) recursively;

d) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b);

e) preparing the variant resulting from steps a) - d);

f) testing the pH dependent activity of said variant; and

5 g) optionally repeating steps a) - f) recursively; and

h) selecting a variant having an altered pH dependent activity as compared to the parent amylase.

20. A method according to any of the preceding claims, wherein the parent pullulanase has more than 40% homology with the amino acid sequence shown in
10 SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5, preferably more than 50%, such as more than 60%, more than 70%, more than 75%, more than 80%, more than 85%, more than 90%, more than 91%, more than 92%, more than 93%, more than 94%, more than 95%, more than 96%, more than 97%, more than 98%, more than 99% homology with the amino acid sequence shown in SEQ ID NO: 1, SEQ ID NO: 3 or
15 SEQ ID NO: 5.

21. A method according to claim 20, wherein the parent pullulanase has the amino acid sequences shown in SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5.

22. A method for producing a pullulanase variant, the method comprising:

- 20 a) constructing the variant by the method according to any of claims 10-21;
- b) transforming a microorganism with a DNA sequence encoding the variant;
- c) cultivating the transformed microorganism under conditions which are conducive for producing the variant; and
- d) optionally, recovering the variant from the resulting culture broth.

23. A pullulanase variant, wherein

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(a) the variant has more than 40% homology to SEQ ID NO:1;

(b) the variant comprises an amino acid modification compared to SEQ ID NO:1 in at least one of the positions corresponding to 95-113, K122P, 130-140, K151P, 157-165, 180, 181, 210, 227, 228, 232-238, 259, 266-272, 286, G293P, 298, 299, 300-314, such as 302-308, N315P, 337-339, 353, N374P, 380, 384, 385, 392, 394, 396, 406, 408-429, such as 418-428, 442, A446P, 478, 500-507, 515, 526, 534, 543, 544 550, T556P, 557, 563, 568, 573, 576, 583, 627, 659-665, G668P, G672P, 681, 684, 688, 689, 751-755, 732, 736, 740, 760, 767, 770 783, 788, 792, 793, such as N793P, K758C+I914C, T916C+A765C, I897C+S819C, P525C+E499C and H286C+T148C;

(c) the variant has an improved thermostability as compared to the parent pullulanase.

24. A pullulanase variant, wherein

(a) the variant has more than 40% homology to SEQ ID NO:1;

(b) the variant comprises an amino acid modification compared to SEQ ID NO:1 in at least one of the positions corresponding to 437, 439, 487, 489, 490, 494-496, 505-511, 514, 551-559, 584-590, 620-626, 650-658, 665-668, 679, 681, 684, 685, 690-693, 731, 734-738, 775, 786, and 789-795;

(c) the variant has an increased isoamylase activity as compared to the parent pullulanase.

25. A pullulanase variant, wherein

(a) the variant has more than 40% homology to SEQ ID NO:1;

(b) the variant comprises an amino acid modification compared to SEQ ID NO: 1 in at least one of the positions corresponding to 430, 433, 435-443, 486-496, 505-515, 518, 521, 548-560, 565, 573-575, 583-595, 599, 600, 602-604, 606-608, 610, 611, 616-633, 635, 636, 639, 646-672, 674-696,

717, 720-722, 725-747, 760, 763, 764, 767, 773-781, 783-797, 799-802 and 817;

(c) the variant has an altered pH dependent activity as compared to the parent pullulanase.

- 5 26. A pullulanase variant according to any of claims 23, 24 or 25, wherein the variant has more than 45% homology with the amino acid sequence shown in SEQ ID NO: 1, preferably more than 50%, such as more than 60%, more than 70%, more than 75%, more than 80%, more than 85%, more than 90%, more than 91%, more than 92%, more than 93%, more than 94%, more than 95%, more than 96%, more than 97%,
10 more than 98%, more than 99% homology with the amino acid sequence shown in SEQ ID NO: 1.

27. A pullulanase variant according to claim 26, wherein the parent pullulanase has the amino acid sequence shown in SEQ ID NO:1.

28. A pullulanase variant, wherein

- 15 (a) the variant has more than 40% homology to SEQ ID NO:3;
- (b) the variant comprises an amino acid modification compared to SEQ ID NO:3 in at least one of the positions corresponding to 111, 112, 158-160, 270-274, 302-314, 392, 400, 408-426, 428, 437, 440, 444, 446, 483, 485, 487, 492, 495, 504, 551, D526P, 530, 543, 566, 613, 621, 710, 717, 735,
20 775, 779, 789, G794P, 823, 855, 891, 892, 437+503 and 674+664;
- (c) the variant has an improved thermostability as compared to the parent pullulanase.

29. A pullulanase variant, wherein

- (a) the variant has more than 40% homology to SEQ ID NO:3;
- 25 (b) the variant comprises an amino acid modification compared to SEQ ID NO:3 in at least one of the positions corresponding to 435, 437, 485, 487,

488, 492-494, 503-509, 512, 549-557, 582-588, 618-624, 648-656, 663-666,
677, 679, 682, 683, 688-691, 729, 732-736, 773, 784, 787-793;

(c) the variant has an increased isoamylase activity as compared to the
parent pullulanase.

5 30. A pullulanase variant, wherein

(a) the variant has more than 40% homology to SEQ ID NO:3;

(b) the variant comprises an amino acid modification compared to SEQ ID
NO: 3 in at least one of the positions corresponding to 428, 431, 433-441,
484-494, 503-513, 516, 519, 546-558, 563, 571-573, 581-593, 597, 598,
10 600-602, 604-606, 608, 609, 614-631, 633, 634, 637, 644-670, 672-694,
715, 718-720, 723-745, 758, 761, 762, 765, 771-779, 781-795, 797-800,
and 815;

(c) (c) the variant has an altered pH dependent activity as compared to the
parent pullulanase.

15 31. A pullulanase variant according to any of claims 28, 29 or 30, wherein the variant
has more than 45% homology with the amino acid sequence shown in SEQ ID NO: 3,
preferably more than 50%, such as more than 60%, more than 70%, more than 75%,
more than 80%, more than 85%, more than 90%, more than 91%, more than 92%,
more than 93%, more than 94%, more than 95%, more than 96%, more than 97%,
20 more than 98%, more than 99% homology with the amino acid sequence shown in
SEQ ID NO: 3.

32. A pullulanase variant according to claim 31, wherein the parent pullulanase has
the amino acid sequence shown in SEQ ID NO:3.

25 33. A variant according to claims 23 or 28, wherein the improved thermostability is
defined by an increased half-life ($T_{1/2}$) of at least about 5%, preferably, at least about
10%, more preferably at least about 15%, more preferably at least about 25%, most

preferably at least about 50%, such as at least about 100%, in the "T_½ assay for liquefaction" described herein, using a pH of 5.0 and a temperature of 95°C.

34. A variant according to claims 23 or 28, wherein the improved thermostability is defined by an increased residual enzyme activity of at least about 5%, preferably, at least about 10%, more preferably at least about 15%, more preferably at least about 25%, most preferably at least about 50%, such as at least about 100%, in the "assay for residual activity after liquefaction" described herein, using a pH of 5.0 and a temperature of 95°C.

35. A variant according to claims 23 or 28, wherein the improved thermostability is defined by an increased half-life (T_½) of at least about 5%, preferably, at least about 10%, more preferably at least about 15%, more preferably at least about 25%, most preferably at least about 50%, such as at least about 100%, in the "T_½ assay for saccharification" described herein, using a pH of 4.5 and a temperature of 70°C.

36. A variant according to claims 23 or 28, wherein the improved thermostability is defined by an increased residual enzyme activity of at least about 5%, preferably, at least about 10%, more preferably at least about 15%, more preferably at least about 25%, most preferably at least about 50%, such as at least about 100%, in the "assay for residual activity after saccharification" described herein, using a pH of 4.5 and a temperature of 63°C.

37. A variant according to claim 36, wherein the "assay for activity for saccharification" described herein, is carried out at a pH of 4.5 and at a temperature of 70°C.

38. A variant according to claims 24 or 29, wherein the increased isoamylase activity is defined by an increase of at least 5% in the number of reducing ends formed in the "assay for isoamylase-like activity" described herein, using 50 mM sodium acetate, a pH of 4.5, 5.0 or 5.5, a temperature of 60°C and when incubated with a 10% w/v rabbit liver glycogen solution for a period of 10 min.

39. A variant according to any of claims 23, 25, 28 or 30, wherein the variant further has an increased isoamylase activity as compared to the parent pullulanase.

40. A variant according to claim 37, wherein the increased isoamylase activity is as defined in claim 38.

41. A variant according to any of claims 24, 25, 28 or 30, wherein the variant further has an improved thermostability as compared to the parent pullulanase.

5 42. A variant according to claim 41, wherein the improved thermostability is as defined in any of claims 33-37.

43. A variant according to any of claims 23, 24, 28 or 29, wherein the variant further has an altered pH dependent activity as compared to the parent pullulanase.

10 44. An isolated nucleic acid sequence comprising a nucleic acid sequence, which encodes for the pullulanase variant defined in any of claims 23-43.

45. An isolated nucleic acid sequence according to claim 44, wherein the nucleic acid sequence is selected from the group consisting of:

(a) a nucleic acid sequence having at least 40% homology with the nucleic acid sequence shown in SEQ ID NO: 1 or SEQ ID NO: 3, and

15 (b) a nucleic acid sequence which hybridizes under low stringency conditions, preferably under medium stringency conditions, in particular under high stringency conditions, with

(i) a complementary strand of the nucleic acid sequence shown in SEQ ID NO: 1 or SEQ ID NO: 3, or

20 (ii) a subsequence of (i) of at least 100 nucleotides.

46. An isolated nucleic acid sequence according to claim 45, wherein the nucleic acid sequence has at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% homology with the nucleic acid sequence shown as SEQ ID NO: 1 or SEQ ID NO:3.

25

47. An isolated nucleic acid construct comprising a nucleic acid sequence as defined in any of claims 44-46, operably linked to one or more control sequences capable of directing the expression of the polypeptide in a suitable expression host.
48. A recombinant expression vector comprising the nucleic acid sequence of claim 5 47, a promoter, and transcriptional and translational stop signals, and preferably further comprising a selectable marker.
49. A recombinant host cell comprising the nucleic acid construct of claim 47.
50. A method for producing the variant defined in any of claims 23-43, the method comprising:
- 10 (a) cultivating the recombinant host cell of claim 49 under conditions conducive to the production of the pullulanase variant; and
- (b) recovering the variant.
51. A method for converting starch to one or more sugars, the method comprising debranching the starch using at least one pullulanase obtained by the methods 15 defined in any of claims 1-22.
52. A method for converting starch to one or more sugars, the method comprising debranching the starch using at least one pullulanase variant as defined in any of claims 23-44.
53. An isolated nucleic acid sequence comprising the nucleic acid sequence shown in 20 SEQ ID NO: 1.
54. A nucleic acid sequence according to claim 53, wherein the isolated nucleic acid sequence consists of the nucleic acid sequence shown in SEQ ID NO: 1.
55. An isolated nucleic acid construct comprising a nucleic acid sequence as defined in claims 53 or 54, operably linked to one or more control sequences capable of 25 directing the expression of the polypeptide in a suitable expression host.

56. A recombinant expression vector comprising the nucleic acid sequence of claim 55, a promoter, and transcriptional and translational stop signals, and preferably further comprising a selectable marker.

57. A recombinant host cell comprising the nucleic acid construct of claim 55.

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The inventors have modified the amino acid sequence of a pullulanase to obtain variants with improved properties, based on the three-dimensional structure of the pullulanase Promozyme®. The variants have altered physicochemical properties., e.g. an altered pH optimum, improved thermostability, altered substrate specificity, increased specific activity or an altered cleavage pattern.

5 e.g. an altered pH optimum, improved thermostability, altered substrate specificity,
increased specific activity or an altered cleavage pattern.

COMBINED DECLARATION FOR PATENT APPLICATION AND POWER OF ATTORNEY
(Includes Reference to PCT International Applications)

Attorney's Docket Number:
6072.200-US

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

Pullulanase Variants and Methods for Preparing Such Variants With Predetermined Properties

The specification of which (check only one item below):

- ☐ is attached hereto
☒ was filed as United States application

Application No. To Be Assigned

on February 28, 2000

and was amended

on _____

☐ was filed as PCT international application

Number _____

on _____

and was amended under PCT Article 19

on _____

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by an amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability of this application in accordance with Title 37, Code of Federal Regulations, §1.56.

I hereby claim priority benefits under Title 35, United States Code, §119 of any provisional or foreign application(s) for patent or inventor's certificate or of any PCT international applications(s) for patent or inventor's certificate or of any PCT international applications(s) designating at least one country other than the United States of America listed below and have also identified below any foreign application(s) for patent or inventor's certificate or any PCT international application(s) designating at least one country other than the United States of America filed by me on the same subject matter having a filing date before that of the application(s) of which priority is claimed:

PRIOR U.S. PROVISIONAL/FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 U.S.C. 119:

COUNTRY (if PCT, indicated "PCT")	APPLICATION NUMBER	DATE OF FILING (day, month, year)	PRIORITY CLAIMED UNDER 35 USC 119	
Denmark	PA 2000 00045	12 January 2000	<input checked="" type="checkbox"/> YES	<input type="checkbox"/> NO
			<input type="checkbox"/> YES	<input type="checkbox"/> NO
			<input type="checkbox"/> YES	<input type="checkbox"/> NO
			<input type="checkbox"/> YES	<input type="checkbox"/> NO
			<input type="checkbox"/> YES	<input type="checkbox"/> NO

Attorney's Docket Number:
6072.200-US

PRIOR U S APPLICATIONS OR PCT INTERNATIONAL APPLICATIONS DESIGNATING THE U S FOR BENEFIT
UNDER 35 U S C 120

POWER OF ATTORNEY As a named inventor, I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and transact all business in the Patent and Trademark Office connected therewith Steve T Zelson Elias J Lambiris Valeta A Gregg Carol E Rozek Robert L Stames Reza Green, Reg No 30,335 Reg No 33,728 Reg No 35,127 Reg No 36,993 Reg No 41,324 Reg No 38,475

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New Form, New Form 10/17/99-01/00				
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3	Full Name of Inventor	Family Name	First Given Name	Second Given Name
	Residence & Citizenship	City	State or Foreign Country	Country of Citizenship
	Post Office Address	Post Office Address	City	State & Zip Code/Country
4	Full Name of Inventor	Family Name	First Given Name	Second Given Name
	Residence & Citizenship	City	State or Foreign Country	Country of Citizenship
	Post Office Address	Post Office Address	City	State & Zip Code/Country

Table 1. *Estimated probabilities of infection from a single contact with a case of influenza A (H1N1) virus infection, by age group and duration of contact*

COMBINED DECLARATION FOR PATENT APPLICATION AND POWER OF ATTORNEY
(Includes Reference to PCT International Applications)

Attorney's Docket Number:

6072.200-US

5	Full Name of Inventor	Family Name	First Given Name	Second Given Name
	Residence & Citizenship	City	State or Foreign Country	Country of Citizenship
	Post Office Address	Post Office Address	City	State & Zip Code/Country
6	Full Name of Inventor	Family Name	First Given Name	Second Given Name
	Residence & Citizenship	City	State or Foreign Country	Country of Citizenship
	Post Office Address	Post Office Address	City	State & Zip Code/Country
7	Full Name of Inventor	Family Name	First Given Name	Second Given Name
	Residence & Citizenship	City	State or Foreign Country	Country of Citizenship
	Post Office Address	Post Office Address	City	State & Zip Code/Country
8	Full Name of Inventor	Family Name	First Given Name	Second Given Name
	Residence & Citizenship	City	State or Foreign Country	Country of Citizenship
	Post Office Address	Post Office Address	City	State & Zip Code/Country
9	Full Name of Inventor	Family Name	First Given Name	Second Given Name
	Residence & Citizenship	City	State or Foreign Country	Country of Citizenship
	Post Office Address	Post Office Address	City	State & Zip Code/Country
<p>I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon</p>				
Signature of Inventor 1		Signature of Inventor 2		Signature of Inventor 3
Date		Date		Date
Signature of Inventor 4		Signature of Inventor 5		Signature of Inventor 6
Date		Date		Date
Signature of Inventor 7		Signature of Inventor 8		Signature of Inventor 9
Date		Date		Date

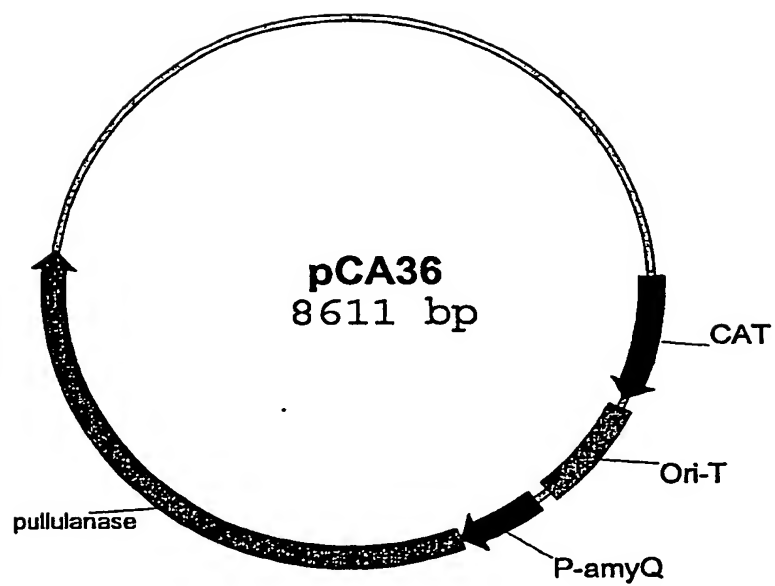


Fig. 1

09514599.022800

Questions and answers about the new law.

<120> Pullulanase variants and methods for preparing such variants with predetermined properties

<140>

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 Asn Tyr Thr Asn Trp Asp Val Trp Met Trp Pro Tyr Gln Pro Val Asn
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Gly Asn Gly Ala Ala Tyr Gln Phe Thr Gly Thr Asn Asp Asp Phe Gly
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Ala Val Ala Asp Thr Gln Val Pro Gly Asp Asn Thr Gln Val Gly Leu
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Ile Val Arg Lys Asn Asp Trp Ser Glu Lys Asn Thr Pro Asn Asp Leu
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His Ile Asp Leu Ala Lys Gly His Glu Val Trp Ile Val Gln Gly Asp

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Ser Val Ser Asn Ala Tyr Leu Asp Asp Glu Lys Thr Val Leu Ala Lys			
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Leu Ser Met Pro Met Thr Leu Ala Asp Ala Ala Ser Gly Phe Thr Val			
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Lys Ile Asn Pro Asn Leu Tyr Gln Leu Ser Gly Thr Leu Pro Ala Gly			
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Thr Tyr Gln Tyr Lys Ile Ala Leu Asp His Ser Trp Asn Thr Ser Tyr			
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Pro Gly Asn Asn Val Ser Leu Thr Val Pro Gln Gly Gly Glu Lys Val			
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690 695 700															
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Phe Ser Ser Met Ile His Leu Arg Asn Gln His Pro Ala Phe Arg Met															
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Thr Asn Thr Val Ala Phe Glu Leu Lys Asn Tyr Ala Asn His Asp Thr															

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Ile Gly Glu Lys Ser Leu Gly His Val Met Gly Asn Val Gln Val Pro			
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Ile Val Arg Lys Asn Asp Trp Ser Glu Lys Asn Thr Pro Asn Asp Leu			
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His Ile Asp Leu Ala Lys Gly His Glu Val Trp Ile Val Gln Gly Asp			
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Ser Val Ser Asn Ala Tyr Leu Asp Asp Glu Lys Thr Val Leu Ala Lys			
115	120		125

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Glu Val Ile Tyr Glu Ala His Val Arg Asp Phe Ser Ile Asp Ala Asn	435	440	445	
Ser Gly Met Lys Asn Lys Gly Lys Tyr Leu Ala Phe Thr Glu His Gly	450	455	460	
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Ala Arg Ile Thr Glu Leu Lys Gln Leu Ile Gln Ser Leu His Gln Gln	530	535	540	
Arg Ile Gly Val Asn Met Asp Val Val Tyr Asn His Thr Phe Asp Val	545	550	555	560
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Ala Ile Ser Thr Leu Ile Leu Lys Gln
915 920

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